

SEQUENCE LISTING

<110> Yale University
Carlson, John R.
Kim, Hunhyong
Clyne, Peter J.
Warr, Coral G.

<120> Novel Family of Odorant Receptor Genes in Drosophila

<130> 44574-5061-US

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<150> US 60/117,132

<151> 1999-01-25

<160> 112

<170> PatentIn Ver. 2.1

<210> 1

<211> 767

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(765)

<223> DOR 22A.2, coding region of NCBI Accession No.
AF127924

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cggttt aag tcc cga gat gcc ttc gtt tac tta gat cgg gtg atg tgg	96
Arg Val Lys Ser Arg Asp Ala Phe Val Tyr Leu Asp Arg Val Met Trp	
20 25 30	
tcc ttt ggc tgg aca gtg cct gaa aac aaa agg tgg gat cta cat tac	144
Ser Phe Gly Trp Thr Val Pro Glu Asn Lys Arg Trp Asp Leu His Tyr	
35 40 45	
aaa ctg tgg tca act ttc gtg aca ttg ttg ata ttt atc ctt ctg ccg	192
Lys Leu Trp Ser Thr Phe Val Thr Leu Leu Ile Phe Ile Leu Leu Pro	
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SEQUENCE LISTING

<110> Yale University
 Carlson, John R.
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<120> Novel Family of Odorant Receptor Genes in Drosophila

<130> 44574-5061-WO

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<150> US 60/117,132

<151> 1999-01-25

<160> 112

<170> PatentIn Ver. 2.1

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<211> 767

<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (1)..(765)

<223> DOR 22A.2, coding region of NCBI Accession No.
 AF127924

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Arg Val Lys Ser Arg Asp Ala Phe Val Tyr Leu Asp Arg Val Met Trp	
20 25 30	
tcc ttt ggc tgg aca gtg cct gaa aac aaa agg tgg gat cta cat tac	144
Ser Phe Gly Trp Thr Val Pro Glu Asn Lys Arg Trp Asp Leu His Tyr	
35 40 45	
aaa ctg tgg tca act ttc gtg aca ttg ttg ata ttt atc ctt ctg ccg	192
Lys Leu Trp Ser Thr Phe Val Thr Leu Leu Ile Phe Ile Leu Leu Pro	
50 55 60	

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Ile Ser Val Ser Val Glu Tyr Ile Gln Arg Phe Lys Thr Phe Ser Ala	
65 70 75 80	
ggt gag ttt ctt agc tca atc cag att ggc gtt aac atg tac gga agc	288
Gly Glu Phe Leu Ser Ser Ile Gln Ile Gly Val Asn Met Tyr Gly Ser	
85 90 95	
agc ttt aaa agt tat ttg acc atg atg gga tat aag aag aga cag gag	336
Ser Phe Lys Ser Tyr Leu Thr Met Met Gly Tyr Lys Lys Arg Gln Glu	
100 105 110	
gct aag atg tca ctg gat gag ctg gac aag aga tgc gtt tgt gat gag	384
Ala Lys Met Ser Leu Asp Glu Leu Asp Lys Arg Cys Val Cys Asp Glu	
115 120 125	
gag agg acc att gta cat cga cat gtc gcc ctg gga aac ttt tgc tat	432
Glu Arg Thr Ile Val His Arg His Val Ala Leu Gly Asn Phe Cys Tyr	
130 135 140	
att ttc tat cac att gcg tac act agc ttt ttg att tca aac ttt ttg	480
Ile Phe Tyr His Ile Ala Tyr Thr Ser Phe Leu Ile Ser Asn Phe Leu	
145 150 155 160	
tca ttt ata atg aag aga atc cat gcc tgg cgc atg tac ttt ccc tac	528
Ser Phe Ile Met Lys Arg Ile His Ala Trp Arg Met Tyr Phe Pro Tyr	
165 170 175	
gtc gac ccc gaa aag caa ttt tac atc tct agc atc gcc gaa gtc att	576
Val Asp Pro Glu Lys Gln Phe Tyr Ile Ser Ser Ile Ala Glu Val Ile	
180 185 190	
ctt agg gga tgg gcc gtc ttc atg gat ctc tgc acg gat gtg tgt cct	624
Leu Arg Gly Trp Ala Val Phe Met Asp Leu Cys Thr Asp Val Cys Pro	
195 200 205	
ttg atc tcc atg gta ata gca cga tgc cac atc acc ctt ctg aaa cag	672
Leu Ile Ser Met Val Ile Ala Arg Cys His Ile Thr Leu Leu Lys Gln	
210 215 220	
cgc ctg cga aat cta cga tcg gaa cca gga agg acg gaa gat gag tac	720
Arg Leu Arg Asn Leu Arg Ser Glu Pro Gly Arg Thr Glu Asp Glu Tyr	
225 230 235 240	
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 <213> Drosophila melanogaster

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Ser	Phe	Gly	Trp	Thr	Val	Pro	Glu	Asn	Lys	Arg	Trp	Asp	Leu	His	Tyr
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Lys	Leu	Trp	Ser	Thr	Phe	Val	Thr	Leu	Leu	Ile	Phe	Ile	Leu	Leu	Pro
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Ile	Ser	Val	Ser	Val	Glu	Tyr	Ile	Gln	Arg	Phe	Lys	Thr	Phe	Ser	Ala
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			85						90					95	
Ser	Phe	Lys	Ser	Tyr	Leu	Thr	Met	Met	Gly	Tyr	Lys	Lys	Arg	Gln	Glu
			100					105					110		
Ala	Lys	Met	Ser	Leu	Asp	Glu	Leu	Asp	Lys	Arg	Cys	Val	Cys	Asp	Glu
		115					120					125			
Glu	Arg	Thr	Ile	Val	His	Arg	His	Val	Ala	Leu	Gly	Asn	Phe	Cys	Tyr
	130					135					140				
Ile	Phe	Tyr	His	Ile	Ala	Tyr	Thr	Ser	Phe	Leu	Ile	Ser	Asn	Phe	Leu
145				150						155					160
Ser	Phe	Ile	Met	Lys	Arg	Ile	His	Ala	Trp	Arg	Met	Tyr	Phe	Pro	Tyr
			165					170					175		
Val	Asp	Pro	Glu	Lys	Gln	Phe	Tyr	Ile	Ser	Ser	Ile	Ala	Glu	Val	Ile
		180						185				190			
Leu	Arg	Gly	Trp	Ala	Val	Phe	Met	Asp	Leu	Cys	Thr	Asp	Val	Cys	Pro
	195						200					205			
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210	215	220
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 <223> DOR 22C.1, a coding segment on BDGP Clone No.
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 Pro Arg Ile Ser Gly Leu Ile Val Gly Leu Trp Pro Gln Arg Ile Arg
 20 25 30

 ggc ggg ggc ggt cgt cct tgg cac gcc cat ctg ctc ttc gtg ttc gcc 144
 Gly Gly Gly Arg Pro Trp His Ala His Leu Leu Phe Val Phe Ala
 35 40 45

 ttc gcc atg gtg gtg gtg ggt gcg gtg ggc gag gtg tcg tac ggc tgt 192
 Phe Ala Met Val Val Val Gly Ala Val Gly Glu Val Ser Tyr Gly Cys
 50 55 60

 gtc cac ctg gac aac ctg gtg gtg gcg ctg gag gcc ttc tgc ccc gga 240
 Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
 65 70 75 80

 acc acc aag gcg gtc tgc gtt ttg aag ctg tgg gtc ttc ttc cgc tcc 288
 Thr Thr Lys Ala Val Cys Val Leu Lys Leu Trp Val Phe Phe Arg Ser
 85 90 95

 aat cgc cgg tgg gcg gag ttg gtc cag cgc ctg cgg gct att ttg ctc 336
 Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Leu

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agc ctg ttg ttg ctc agc tct ggc acg gcg aca aat gcc gcc ttc acc			384
Ser Leu Leu Leu Leu Ser Ser Gly Thr Ala Thr Asn Ala Ala Phe Thr			
115	120	125	
ttg caa ccg ctg att atg ggt ctc tac cgc tgg att gtg cag ctg cca			432
Leu Gln Pro Leu Ile Met Gly Leu Tyr Arg Trp Ile Val Gln Leu Pro			
130	135	140	
ggt caa acc gag ctg ccc ttt aat atc ata ctg ccc tcg ttt gcc gtg			480
Gly Gln Thr Glu Leu Pro Phe Asn Ile Ile Leu Pro Ser Phe Ala Val			
145	150	155	160
cag cca gga gtc ttt ccg ctc acc tac gtg ctg ctg acc gct tcc ggt			528
Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu Leu Thr Ala Ser Gly			
165	170	175	
gcc tgc acc gtt ttc gcc ttc agc ttc gtg gac gga ttc ttc att tgc			576
Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp Gly Phe Phe Ile Cys			
180	185	190	
tcg tgc ctc tac atc tgc ggc gct ttc cgg ctg gtg cag cag gac att			624
Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu Val Gln Gln Asp Ile			
195	200	205	
cgc agg ata ttt gcc gat ttg cat ggc gtg gat gtg ttc acc gag gag			672
Arg Arg Ile Phe Ala Asp Leu His Gly Val Asp Val Phe Thr Glu Glu			
210	215	220	
atg aac gcg gag gtg cgg cac aga ctg gcc caa gtt gtc gag cgg cac			720
Met Asn Ala Glu Val Arg His Arg Leu Ala Gln Val Val Glu Arg His			
225	230	235	240
aat gcg att atc gat ttc tgc acg gac cta aca cgc cag ttc acc gtt			768
Asn Ala Ile Ile Asp Phe Cys Thr Asp Leu Thr Arg Gln Phe Thr Val			
245	250	255	
atc gtt tta atg cat ttc ctg tcc gcc gcc ttc gtc ctc tgc tcg acc			816
Ile Val Leu Met His Phe Leu Ser Ala Ala Phe Val Leu Cys Ser Thr			
260	265	270	
atc ctg gac atc atg ttg aac acg tcg tcg ttg agc ggc tta acc tac			864
Ile Leu Asp Ile Met Leu Asn Thr Ser Ser Leu Ser Gly Leu Thr Tyr			
275	280	285	
atc tgc tat atc atc gcg gcc cta acg cag cta ttc ctc tac tgc ttc			912
Ile Cys Tyr Ile Ile Ala Ala Leu Thr Gln Leu Phe Leu Tyr Cys Phe			

290	295	300	
gga ggc aat cac gtc agc gag agt agt gcg gct gtg gcg gac gtg ctg			960
Gly Gly Asn His Val Ser Glu Ser Ser Ala Ala Val Ala Asp Val Leu			
305	310	315	320
tac gac atg gag tgg tac aaa tgc gat gcg agg act agg aaa gtg att			1008
Tyr Asp Met Glu Trp Tyr Lys Cys Asp Ala Arg Thr Arg Lys Val Ile			
	325	330	335
tta atg ata ttg cgc cgt tcg cag cgg gca aaa aca att gcg gtg ccg			1056
Leu Met Ile Leu Arg Arg Ser Gln Arg Ala Lys Thr Ile Ala Val Pro			
	340	345	350
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Phe Phe Thr Pro Ser Leu Pro Ala Leu Arg Ser Ile Leu Ser Thr Ala			
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			20					25					30		
Gly	Gly	Gly	Gly	Arg	Pro	Trp	His	Ala	His	Leu	Leu	Phe	Val	Phe	Ala
			35				40						45		
Phe	Ala	Met	Val	Val	Val	Gly	Ala	Val	Gly	Glu	Val	Ser	Tyr	Gly	Cys
	50					55					60				
Val	His	Leu	Asp	Asn	Leu	Val	Val	Ala	Leu	Glu	Ala	Phe	Cys	Pro	Gly
	65				70					75					80
Thr	Thr	Lys	Ala	Val	Cys	Val	Leu	Lys	Leu	Trp	Val	Phe	Phe	Arg	Ser
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Asn	Arg	Arg	Trp	Ala	Glu	Leu	Val	Gln	Arg	Leu	Arg	Ala	Ile	Leu	Leu

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145	150	155
Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu Leu Thr Ala Ser Gly		
	165	170
Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp Gly Phe Phe Ile Cys		
	180	185
Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu Val Gln Gln Asp Ile		
195	200	205
Arg Arg Ile Phe Ala Asp Leu His Gly Val Asp Val Phe Thr Glu Glu		
210	215	220
Met Asn Ala Glu Val Arg His Arg Leu Ala Gln Val Val Glu Arg His		
225	230	235
Asn Ala Ile Ile Asp Phe Cys Thr Asp Leu Thr Arg Gln Phe Thr Val		
	245	250
Ile Val Leu Met His Phe Leu Ser Ala Ala Phe Val Leu Cys Ser Thr		
	260	265
Ile Leu Asp Ile Met Leu Asn Thr Ser Ser Leu Ser Gly Leu Thr Tyr		
275	280	285
Ile Cys Tyr Ile Ile Ala Ala Leu Thr Gln Leu Phe Leu Tyr Cys Phe		
290	295	300
Gly Gly Asn His Val Ser Glu Ser Ser Ala Ala Val Ala Asp Val Leu		
305	310	315
Tyr Asp Met Glu Trp Tyr Lys Cys Asp Ala Arg Thr Arg Lys Val Ile		
	325	330
Leu Met Ile Leu Arg Arg Ser Gln Arg Ala Lys Thr Ile Ala Val Pro		
	340	345
Phe Phe Thr Pro Ser Leu Pro Ala Leu Arg Ser Ile Leu Ser Thr Ala		

355

360

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Gly Ser Tyr Ile Thr Leu Leu Lys Thr Phe Leu
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<211> 1140

<212> DNA

<213> *Drosophila melanogaster*

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aat gcc tgg cga att tgt ggt gcc ttg gat ctc agc gag ggt agg tac 96
 Asn Ala Trp Arg Ile Cys Gly Ala Leu Asp Leu Ser Glu Gly Arg Tyr
 20 25 30

tgg agt tgg tcg atg cta ttg tgc atc ttg gtg tac ctg ccg aca ccc 144
 Trp Ser Trp Ser Met Leu Leu Cys Ile Leu Val Tyr Leu Pro Thr Pro
 35 40 45

atg cta ctg aga gga gta tac agt ttc gaa gat ccg gtg gaa aat aat 192
 Met Leu Leu Arg Gly Val Tyr Ser Phe Glu Asp Pro Val Glu Asn Asn
 50 55 60

ttc agc ttg agc ctg acg gtc act tcg ctg tcc aat ctc atg aag ttc 240
 Phe Ser Leu Ser Leu Thr Val Thr Ser Leu Ser Asn Leu Met Lys Phe
 65 70 75 80

tgc atg tac gtg gcc caa cta aca aag atg gtc gag gtc cag agt ctt 288
 Cys Met Tyr Val Ala Gln Leu Thr Lys Met Val Glu Val Gln Ser Leu
 85 90 95

att ggt cag ctg gat gcc cgg gtt tct ggc gag agc cag tct gag cgt 336
 Ile Gly Gln Leu Asp Ala Arg Val Ser Gly Glu Ser Gln Ser Glu Arg
 100 105 110

cat aga aat atg acc gag cac ctg cta agg atg tcc aag ctg ttc cag 384
 His Arg Asn Met Thr Glu His Leu Leu Arg Met Ser Lys Leu Phe Gln

115	120	125	
atc acc tac gct gta gtc ttc atc att gct gca gtt ccc ttc gtt ttc			432
Ile Thr Tyr Ala Val Val Phe Ile Ile Ala Ala Val Pro Phe Val Phe			
130	135	140	
gaa act gag cta agc tta ccc atg ccc atg tgg ttt ccc ttc gac tgg			480
Glu Thr Glu Leu Ser Leu Pro Met Pro Met Trp Phe Pro Phe Asp Trp			
145	150	155	160
aag aac tcg atg gtg gcc tac atc gga gct ctg gtt ttc cag gag att			528
Lys Asn Ser Met Val Ala Tyr Ile Gly Ala Leu Val Phe Gln Glu Ile			
165	170	175	
ggc tat gtc ttt caa att atg caa tgc ttt gca gct gac tcg ttt ccc			576
Gly Tyr Val Phe Gln Ile Met Gln Cys Phe Ala Ala Asp Ser Phe Pro			
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ccg ctc gta ctg tac ctg atc tcc gag caa tgt caa ttg ctg atc ctg			624
Pro Leu Val Leu Tyr Leu Ile Ser Glu Gln Cys Gln Leu Leu Ile Leu			
195	200	205	
aga atc tct gaa atc gga tat ggt tac aag act ctg gag gag aac gaa			672
Arg Ile Ser Glu Ile Gly Tyr Gly Tyr Lys Thr Leu Glu Glu Asn Glu			
210	215	220	
cag gat ctg gtc aac tgc atc agg gat caa aac gcg ctg tat aga tta			720
Gln Asp Leu Val Asn Cys Ile Arg Asp Gln Asn Ala Leu Tyr Arg Leu			
225	230	235	240
ctc gat gtg acc aag agt ctc gtt tcg tat ccc atg atg gtg cag ttt			768
Leu Asp Val Thr Lys Ser Leu Val Ser Tyr Pro Met Met Val Gln Phe			
245	250	255	
atg gtt att ggc atc aac atc gcc atc acc cta ttt gtc ctg ata ttt			816
Met Val Ile Gly Ile Asn Ile Ala Ile Thr Leu Phe Val Leu Ile Phe			
260	265	270	
tac gtg gag acc ttg tac gat cgc atc tat tat ctt tgc ttt ctc ttg			864
Tyr Val Glu Thr Leu Tyr Asp Arg Ile Tyr Tyr Leu Cys Phe Leu Leu			
275	280	285	
ggc atc acc gtg cag aca tat cca ttg tgc tac tat gga acc atg gtg			912
Gly Ile Thr Val Gln Thr Tyr Pro Leu Cys Tyr Tyr Gly Thr Met Val			
290	295	300	
cag gag agt ttt gct gag ctt cac tat gcg gta ttc tgc agc aac tgg			960
Gln Glu Ser Phe Ala Glu Leu His Tyr Ala Val Phe Cys Ser Asn Trp			

305	310	315	320	
gtg gat caa agt gcc agc tat cgt ggg cac atg ctc atc ctg gcg gag				1008
Val Asp Gln Ser Ala Ser Tyr Arg Gly His Met Leu Ile Leu Ala Glu				
	325	330	335	
cgc act aag cgg atg cag ctt ctc ctc gcc ggc aac ctg gtg ccc atc				1056
Arg Thr Lys Arg Met Gln Leu Leu Leu Ala Gly Asn Leu Val Pro Ile				
	340	345	350	
cac ctg agc acc tac gtg gcc tgt tgg aag gga gcc tac tcc ttc ttc				1104
His Leu Ser Thr Tyr Val Ala Cys Trp Lys Gly Ala Tyr Ser Phe Phe				
	355	360	365	
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Trp Ser Trp Ser Met Leu Leu Cys Ile Leu Val Tyr Leu Pro Thr Pro				
	35	40	45	
Met Leu Leu Arg Gly Val Tyr Ser Phe Glu Asp Pro Val Glu Asn Asn				
	50	55	60	
Phe Ser Leu Ser Leu Thr Val Thr Ser Leu Ser Asn Leu Met Lys Phe				
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His Arg Asn Met Thr Glu His Leu Leu Arg Met Ser Lys Leu Phe Gln				
	115	120	125	

Ile Thr Tyr Ala Val Val Phe Ile Ile Ala Ala Val Pro Phe Val Phe
 130 135 140

Glu Thr Glu Leu Ser Leu Pro Met Pro Met Trp Phe Pro Phe Asp Trp
 145 150 155 160

Lys Asn Ser Met Val Ala Tyr Ile Gly Ala Leu Val Phe Gln Glu Ile
 165 170 175

Gly Tyr Val Phe Gln Ile Met Gln Cys Phe Ala Ala Asp Ser Phe Pro
 180 185 190

Pro Leu Val Leu Tyr Leu Ile Ser Glu Gln Cys Gln Leu Leu Ile Leu
 195 200 205

Arg Ile Ser Glu Ile Gly Tyr Gly Tyr Lys Thr Leu Glu Glu Asn Glu
 210 215 220

Gln Asp Leu Val Asn Cys Ile Arg Asp Gln Asn Ala Leu Tyr Arg Leu
 225 230 235 240

Leu Asp Val Thr Lys Ser Leu Val Ser Tyr Pro Met Met Val Gln Phe
 245 250 255

Met Val Ile Gly Ile Asn Ile Ala Ile Thr Leu Phe Val Leu Ile Phe
 260 265 270

Tyr Val Glu Thr Leu Tyr Asp Arg Ile Tyr Tyr Leu Cys Phe Leu Leu
 275 280 285

Gly Ile Thr Val Gln Thr Tyr Pro Leu Cys Tyr Tyr Gly Thr Met Val
 290 295 300

Gln Glu Ser Phe Ala Glu Leu His Tyr Ala Val Phe Cys Ser Asn Trp
 305 310 315 320

Val Asp Gln Ser Ala Ser Tyr Arg Gly His Met Leu Ile Leu Ala Glu
 325 330 335

Arg Thr Lys Arg Met Gln Leu Leu Leu Ala Gly Asn Leu Val Pro Ile
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His Leu Ser Thr Tyr Val Ala Cys Trp Lys Gly Ala Tyr Ser Phe Phe
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Thr Leu Met Ala Asp Arg Asp Gly Leu Gly Ser
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 Phe Met Val Pro Lys Phe Ala Leu Ser Leu Ile Gly Phe Tyr Pro Glu
 20 25 30
 cag aag cga acg gtt ttg gtg aaa ctt tgg agt ttc ttc aac ttt ttc 144
 Gln Lys Arg Thr Val Leu Val Lys Leu Trp Ser Phe Phe Asn Phe Phe
 35 40 45
 atc ctc acc tac ggc tgt tat gca gag gct tac tat ggc ata cac tat 192
 Ile Leu Thr Tyr Gly Cys Tyr Ala Glu Ala Tyr Tyr Gly Ile His Tyr
 50 55 60
 ata ccg att aac ata gcc act gca ttg gat gcc ctt tgt cct gtg gcc 240
 Ile Pro Ile Asn Ile Ala Thr Ala Leu Asp Ala Leu Cys Pro Val Ala
 65 70 75 80
 tcc agc att ttg tcg ctg gtg aaa atg gtc gcc att tgg tgg tat caa 288
 Ser Ser Ile Leu Ser Leu Val Lys Met Val Ala Ile Trp Trp Tyr Gln
 85 90 95
 gat gaa tta agg agt ttg ata gag cgg agg ttc tat aca ctg gca acg 336
 Asp Glu Leu Arg Ser Leu Ile Glu Arg Arg Phe Tyr Thr Leu Ala Thr
 100 105 110
 caa cta aca ttc ctg cta cta tgc tgt gga ttt tgc acc agt act tcc 384
 Gln Leu Thr Phe Leu Leu Leu Cys Cys Gly Phe Cys Thr Ser Thr Ser
 115 120 125
 tat tcc gtc aga cat ttg att gat aat atc ctg aga cgc acc cat ggc 432

Tyr	Ser	Val	Arg	His	Leu	Ile	Asp	Asn	Ile	Leu	Arg	Arg	Thr	His	Gly		
130						135				140							
aag	gac	tgg	atc	tac	gag	act	ccg	ttc	aag	atg	atg	ttc	ccc	gat	ctt	480	
Lys	Asp	Trp	Ile	Tyr	Glu	Thr	Pro	Phe	Lys	Met	Met	Phe	Pro	Asp	Leu		
145					150				155						160		
ctc	ctg	cgt	ttg	cca	ctc	tat	ccc	atc	acc	tat	ata	ctc	gtg	cat	tgg	528	
Leu	Leu	Arg	Leu	Pro	Leu	Tyr	Pro	Ile	Thr	Tyr	Ile	Leu	Val	His	Trp		
				165					170					175			
cat	ggc	tac	att	act	gtg	gtt	tgt	ttt	gtc	ggc	gcg	gat	ggg	ttc	ttc	576	
His	Gly	Tyr	Ile	Thr	Val	Val	Cys	Phe	Val	Gly	Ala	Asp	Gly	Phe	Phe		
			180					185					190				
ctg	ggg	ttc	tgt	ttg	tac	ttc	act	gtt	ttg	ctg	ctc	tgt	ctg	cag	gac	624	
Leu	Gly	Phe	Cys	Leu	Tyr	Phe	Thr	Val	Leu	Leu	Leu	Cys	Leu	Gln	Asp		
		195					200					205					
gat	gtt	tgt	gat	tta	cta	gag	gtt	gaa	aac	atc	gag	aag	agt	ccc	tcc	672	
Asp	Val	Cys	Asp	Leu	Leu	Glu	Val	Glu	Asn	Ile	Glu	Lys	Ser	Pro	Ser		
	210					215					220						
gaa	gcg	gag	gaa	gct	cgc	ata	gtt	cgg	gaa	atg	gaa	aaa	ctg	gtg	gac	720	
Glu	Ala	Glu	Glu	Ala	Arg	Ile	Val	Arg	Glu	Met	Glu	Lys	Leu	Val	Asp		
225				230					235						240		
cgg	cat	aac	gag	gtg	gcc	gag	ctg	aca	gaa	aga	ttg	tcg	ggg	gtt	atg	768	
Arg	His	Asn	Glu	Val	Ala	Glu	Leu	Thr	Glu	Arg	Leu	Ser	Gly	Val	Met		
			245					250					255				
gtg	gaa	ata	aca	ctg	gcc	cac	ttt	gtt	act	tcg	agt	ttg	ata	atc	gga	816	
Val	Glu	Ile	Thr	Leu	Ala	His	Phe	Val	Thr	Ser	Ser	Leu	Ile	Ile	Gly		
			260					265					270				
acc	agc	gtg	gtg	gat	att	tta	tta	ttt	tcc	ggc	ctg	gga	atc	att	gtg	864	
Thr	Ser	Val	Val	Asp	Ile	Leu	Leu	Phe	Ser	Gly	Leu	Gly	Ile	Ile	Val		
		275					280					285					
tat	gtg	gtc	tac	act	tgt	gcc	gta	ggg	gtg	gaa	ata	ttt	cta	tac	tgt	912	
Tyr	Val	Val	Tyr	Thr	Cys	Ala	Val	Gly	Val	Glu	Ile	Phe	Leu	Tyr	Cys		
	290					295					300						
tta	gga	gga	tct	cat	att	atg	gaa	gcg	tgt	tcc	aat	cta	gcg	cgc	tcc	960	
Leu	Gly	Gly	Ser	His	Ile	Met	Glu	Ala	Cys	Ser	Asn	Leu	Ala	Arg	Ser		
305					310				315						320		
aca	ttt	tcc	agc	cac	tgg	tat	ggc	cac	agt	gtt	cgg	gtc	caa	aag	atg	1008	

Thr Phe Ser Ser His Trp Tyr Gly His Ser Val Arg Val Gln Lys Met
 325 330 335

acc ctt ttg atg gta gct cgt gct caa cga gtt ctc aca att aaa att 1056
 Thr Leu Leu Met Val Ala Arg Ala Gln Arg Val Leu Thr Ile Lys Ile
 340 345 350

cct ttc ttt tcc cca tca tta gag act cta act tcg att ttg cgc ttc 1104
 Pro Phe Phe Ser Pro Ser Leu Glu Thr Leu Thr Ser Ile Leu Arg Phe
 355 360 365

act gga tct ctg att gcc ctg gca aag tcg gtt ata taa 1143
 Thr Gly Ser Leu Ile Ala Leu Ala Lys Ser Val Ile
 370 375 380

<210> 8

<211> 380

<212> PRT

<213> Drosophila melanogaster

<400> 8

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Phe Met Val Pro Lys Phe Ala Leu Ser Leu Ile Gly Phe Tyr Pro Glu
 20 25 30

Gln Lys Arg Thr Val Leu Val Lys Leu Trp Ser Phe Phe Asn Phe Phe
 35 40 45

Ile Leu Thr Tyr Gly Cys Tyr Ala Glu Ala Tyr Tyr Gly Ile His Tyr
 50 55 60

Ile Pro Ile Asn Ile Ala Thr Ala Leu Asp Ala Leu Cys Pro Val Ala
 65 70 75 80

Ser Ser Ile Leu Ser Leu Val Lys Met Val Ala Ile Trp Trp Tyr Gln
 85 90 95

Asp Glu Leu Arg Ser Leu Ile Glu Arg Arg Phe Tyr Thr Leu Ala Thr
 100 105 110

Gln Leu Thr Phe Leu Leu Leu Cys Cys Gly Phe Cys Thr Ser Thr Ser
 115 120 125

Tyr Ser Val Arg His Leu Ile Asp Asn Ile Leu Arg Arg Thr His Gly
 130 135 140

Lys Asp Trp Ile Tyr Glu Thr Pro Phe Lys Met Met Phe Pro Asp Leu
 145 150 155 160
 Leu Leu Arg Leu Pro Leu Tyr Pro Ile Thr Tyr Ile Leu Val His Trp
 165 170 175
 His Gly Tyr Ile Thr Val Val Cys Phe Val Gly Ala Asp Gly Phe Phe
 180 185 190
 Leu Gly Phe Cys Leu Tyr Phe Thr Val Leu Leu Leu Cys Leu Gln Asp
 195 200 205
 Asp Val Cys Asp Leu Leu Glu Val Glu Asn Ile Glu Lys Ser Pro Ser
 210 215 220
 Glu Ala Glu Glu Ala Arg Ile Val Arg Glu Met Glu Lys Leu Val Asp
 225 230 235 240
 Arg His Asn Glu Val Ala Glu Leu Thr Glu Arg Leu Ser Gly Val Met
 245 250 255
 Val Glu Ile Thr Leu Ala His Phe Val Thr Ser Ser Leu Ile Ile Gly
 260 265 270
 Thr Ser Val Val Asp Ile Leu Leu Phe Ser Gly Leu Gly Ile Ile Val
 275 280 285
 Tyr Val Val Tyr Thr Cys Ala Val Gly Val Glu Ile Phe Leu Tyr Cys
 290 295 300
 Leu Gly Gly Ser His Ile Met Glu Ala Cys Ser Asn Leu Ala Arg Ser
 305 310 315 320
 Thr Phe Ser Ser His Trp Tyr Gly His Ser Val Arg Val Gln Lys Met
 325 330 335
 Thr Leu Leu Met Val Ala Arg Ala Gln Arg Val Leu Thr Ile Lys Ile
 340 345 350
 Pro Phe Phe Ser Pro Ser Leu Glu Thr Leu Thr Ser Ile Leu Arg Phe
 355 360 365
 Thr Gly Ser Leu Ile Ala Leu Ala Lys Ser Val Ile
 370 375 380

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 <211> 1212
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 <213> *Drosophila melanogaster*

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 <222> (1)..(1209)

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 Met Phe Gly His Phe Lys Leu Val Tyr Pro Ala Pro Ile Ser Glu Pro
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ata cag tct agg gat tcg aat gca tac atg atg gag acg ctg cga aat 96
 Ile Gln Ser Arg Asp Ser Asn Ala Tyr Met Met Glu Thr Leu Arg Asn
 20 25 30

tcg ggc ttg aat ttg aag aac gat ttc ggt ata ggc cgc aag att tgg 144
 Ser Gly Leu Asn Leu Lys Asn Asp Phe Gly Ile Gly Arg Lys Ile Trp
 35 40 45

agg gtg ttt tcg ttc acc tac aat atg gtg ata ctt ccc gta agt ttc 192
 Arg Val Phe Ser Phe Thr Tyr Asn Met Val Ile Leu Pro Val Ser Phe
 50 55 60

cca atc aac tat gtg ata cat ctg gcg gag ttc ccg ccg gag ctg ctg 240
 Pro Ile Asn Tyr Val Ile His Leu Ala Glu Phe Pro Pro Glu Leu Leu
 65 70 75 80

ctg caa tcc ctg caa ctg tgc ctc aac act tgg tgc ttc gct ctg aag 288
 Leu Gln Ser Leu Gln Leu Cys Leu Asn Thr Trp Cys Phe Ala Leu Lys
 85 90 95

ttc ttc act ctg atc gtc tat acg cac cgc ttg gag ctg gcc aac aag 336
 Phe Phe Thr Leu Ile Val Tyr Thr His Arg Leu Glu Leu Ala Asn Lys
 100 105 110

cac ttt gac gaa ttg gat aag tac tgc gtg aag ccg gcg gag aag cgc 384
 His Phe Asp Glu Leu Asp Lys Tyr Cys Val Lys Pro Ala Glu Lys Arg
 115 120 125

aag gtt cgc gac atg gtg gcc act att aca aga ctg tac ctg acc ttc 432
 Lys Val Arg Asp Met Val Ala Thr Ile Thr Arg Leu Tyr Leu Thr Phe
 130 135 140

gtc gtg gtc tac gtc ctc tac gcc acc tcc acg cta ctg gac gga cta 480
 Val Val Val Tyr Val Leu Tyr Ala Thr Ser Thr Leu Leu Asp Gly Leu

145	150	155	160	
ctg cac cac cgt gtt ccc tac aat acg tac tat ccg ttc ata aac tgg				528
Leu His His Arg Val Pro Tyr Asn Thr Tyr Tyr Pro Phe Ile Asn Trp				
	165	170	175	
cga gtc gat cgg acc cag atg tac atc cag agt ttt ctg gag tac ttc				576
Arg Val Asp Arg Thr Gln Met Tyr Ile Gln Ser Phe Leu Glu Tyr Phe				
	180	185	190	
acc gtg ggt tat gcc ata tat gtg gcc acc gcc acc gat tcc tac cct				624
Thr Val Gly Tyr Ala Ile Tyr Val Ala Thr Ala Thr Asp Ser Tyr Pro				
	195	200	205	
gtg att tac gtg gca gcc ctg cga act cat att ctc ttg ctc aag gac				672
Val Ile Tyr Val Ala Ala Leu Arg Thr His Ile Leu Leu Leu Lys Asp				
	210	215	220	
cgt atc att tac ttg ggc gat ccc agc aac gag ggt agc agc gac ccg				720
Arg Ile Ile Tyr Leu Gly Asp Pro Ser Asn Glu Gly Ser Ser Asp Pro				
	225	230	235	240
agc tac atg ttt aaa tcg ttg gtg gat tgt atc aag gca cac aga acc				768
Ser Tyr Met Phe Lys Ser Leu Val Asp Cys Ile Lys Ala His Arg Thr				
	245	250	255	
atg cta aat ttt tgt gat gcc att caa cca atc atc tct ggc acg ata				816
Met Leu Asn Phe Cys Asp Ala Ile Gln Pro Ile Ile Ser Gly Thr Ile				
	260	265	270	
ttt gcc caa ttc atc ata tgc gga tcg atc ctg ggc ata att atg atc				864
Phe Ala Gln Phe Ile Ile Cys Gly Ser Ile Leu Gly Ile Ile Met Ile				
	275	280	285	
aac atg gta ttg ttc gct gat caa tcg acc cga ttc ggc ata gtc atc				912
Asn Met Val Leu Phe Ala Asp Gln Ser Thr Arg Phe Gly Ile Val Ile				
	290	295	300	
tac gtt atg gcc gtc ctt ctg cag act ttt ccg ctt tgc ttc tac tgc				960
Tyr Val Met Ala Val Leu Leu Gln Thr Phe Pro Leu Cys Phe Tyr Cys				
	305	310	315	320
aac gcc atc gtg gac gac tgc aaa gaa ctg gcc cac gca ctt ttc cat				1008
Asn Ala Ile Val Asp Asp Cys Lys Glu Leu Ala His Ala Leu Phe His				
	325	330	335	
tcc gcc tgg tgg gtg cag gac aag cga tac cag cgg act gtc atc cag				1056
Ser Ala Trp Trp Val Gln Asp Lys Arg Tyr Gln Arg Thr Val Ile Gln				

340	345	350	
ttc ctg cag aaa ctg cag cag ccc atg acc ttc acc gcc atg aac ata			1104
Phe Leu Gln Lys Leu Gln Gln Pro Met Thr Phe Thr Ala Met Asn Ile			
355	360	365	
ttt aac att aat ttg gcc act aac atc aat gta gcc aag ttc gcc ttc			1152
Phe Asn Ile Asn Leu Ala Thr Asn Ile Asn Val Ala Lys Phe Ala Phe			
370	375	380	
acc gtg tac gcc atc gcg agc ggt atg aac ctg gac caa aag tta agc			1200
Thr Val Tyr Ala Ile Ala Ser Gly Met Asn Leu Asp Gln Lys Leu Ser			
385	390	395	400
att aag gaa tag			1212
Ile Lys Glu			

<210> 10

<211> 403

<212> PRT

<213> *Drosophila melanogaster*

<400> 10

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Ile	Gln	Ser	Arg	Asp	Ser	Asn	Ala	Tyr	Met	Met	Glu	Thr	Leu	Arg	Asn
			20					25					30		

Ser	Gly	Leu	Asn	Leu	Lys	Asn	Asp	Phe	Gly	Ile	Gly	Arg	Lys	Ile	Trp
		35					40					45			

Arg	Val	Phe	Ser	Phe	Thr	Tyr	Asn	Met	Val	Ile	Leu	Pro	Val	Ser	Phe
	50					55					60				

Pro	Ile	Asn	Tyr	Val	Ile	His	Leu	Ala	Glu	Phe	Pro	Pro	Glu	Leu	Leu
65					70					75				80	

Leu	Gln	Ser	Leu	Gln	Leu	Cys	Leu	Asn	Thr	Trp	Cys	Phe	Ala	Leu	Lys
				85					90					95	

Phe	Phe	Thr	Leu	Ile	Val	Tyr	Thr	His	Arg	Leu	Glu	Leu	Ala	Asn	Lys
			100					105					110		

His	Phe	Asp	Glu	Leu	Asp	Lys	Tyr	Cys	Val	Lys	Pro	Ala	Glu	Lys	Arg
		115					120						125		

Lys Val Arg Asp Met Val Ala Thr Ile Thr Arg Leu Tyr Leu Thr Phe
 130 135 140

Val Val Val Tyr Val Leu Tyr Ala Thr Ser Thr Leu Leu Asp Gly Leu
 145 150 155 160

Leu His His Arg Val Pro Tyr Asn Thr Tyr Tyr Pro Phe Ile Asn Trp
 165 170 175

Arg Val Asp Arg Thr Gln Met Tyr Ile Gln Ser Phe Leu Glu Tyr Phe
 180 185 190

Thr Val Gly Tyr Ala Ile Tyr Val Ala Thr Ala Thr Asp Ser Tyr Pro
 195 200 205

Val Ile Tyr Val Ala Ala Leu Arg Thr His Ile Leu Leu Leu Lys Asp
 210 215 220

Arg Ile Ile Tyr Leu Gly Asp Pro Ser Asn Glu Gly Ser Ser Asp Pro
 225 230 235 240

Ser Tyr Met Phe Lys Ser Leu Val Asp Cys Ile Lys Ala His Arg Thr
 245 250 255

Met Leu Asn Phe Cys Asp Ala Ile Gln Pro Ile Ile Ser Gly Thr Ile
 260 265 270

Phe Ala Gln Phe Ile Ile Cys Gly Ser Ile Leu Gly Ile Ile Met Ile
 275 280 285

Asn Met Val Leu Phe Ala Asp Gln Ser Thr Arg Phe Gly Ile Val Ile
 290 295 300

Tyr Val Met Ala Val Leu Leu Gln Thr Phe Pro Leu Cys Phe Tyr Cys
 305 310 315 320

Asn Ala Ile Val Asp Asp Cys Lys Glu Leu Ala His Ala Leu Phe His
 325 330 335

Ser Ala Trp Trp Val Gln Asp Lys Arg Tyr Gln Arg Thr Val Ile Gln
 340 345 350

Phe Leu Gln Lys Leu Gln Gln Pro Met Thr Phe Thr Ala Met Asn Ile
 355 360 365

Phe Asn Ile Asn Leu Ala Thr Asn Ile Asn Val Ala Lys Phe Ala Phe
 370 375 380

Thr Val Tyr Ala Ile Ala Ser Gly Met Asn Leu Asp Gln Lys Leu Ser
 385 390 395 400

Ile Lys Glu

<210> 11

<211> 1137

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1134)

<223> DOR 33B.1, a coding region on BDGP Clone No.
 AC006240

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tgg ctt tac tgg cga ctt ctg gga gtc gag ggc gat tat cct ttt cga 96
 Trp Leu Tyr Trp Arg Leu Leu Gly Val Glu Gly Asp Tyr Pro Phe Arg
 20 25 30

cgg cta gtg gat ttt aca atc acg tct ttc att acg att tta ttt ccc 144
 Arg Leu Val Asp Phe Thr Ile Thr Ser Phe Ile Thr Ile Leu Phe Pro
 35 40 45

gtg cat ctt ata ctg gga atg tat aaa aag ccc cag att caa gtc ttc 192
 Val His Leu Ile Leu Gly Met Tyr Lys Lys Pro Gln Ile Gln Val Phe
 50 55 60

agg agt ctg cat ttc aca tcg gaa tgc ctt ttc tgc agc tat aag ttt 240
 Arg Ser Leu His Phe Thr Ser Glu Cys Leu Phe Cys Ser Tyr Lys Phe
 65 70 75 80

ttc tgt ttt cgt tgg aaa ctt aaa gaa ata aag acc atc gaa gga ttg 288
 Phe Cys Phe Arg Trp Lys Leu Lys Glu Ile Lys Thr Ile Glu Gly Leu
 85 90 95

ctc cag gat ctc gat agt cga gtt gaa agt gaa gaa gaa cgc aac tac 336
 Leu Gln Asp Leu Asp Ser Arg Val Glu Ser Glu Glu Glu Arg Asn Tyr
 100 105 110

ttt aat caa aat cca agt cgt gtg gct cga atg ctt tcg aaa agt tac	384
Phe Asn Gln Asn Pro Ser Arg Val Ala Arg Met Leu Ser Lys Ser Tyr	
115 120 125	
ttg gta gct gct ata tcg gcc ata atc act gca act gta gct ggt tta	432
Leu Val Ala Ala Ile Ser Ala Ile Ile Thr Ala Thr Val Ala Gly Leu	
130 135 140	
ttt agt act ggt cga aat tta atg tat ctg ggt tgg ttt ccc tac gat	480
Phe Ser Thr Gly Arg Asn Leu Met Tyr Leu Gly Trp Phe Pro Tyr Asp	
145 150 155 160	
ttt caa gca acc gcc gca atc tat tgg att agt ttt tcc tat cag gcg	528
Phe Gln Ala Thr Ala Ala Ile Tyr Trp Ile Ser Phe Ser Tyr Gln Ala	
165 170 175	
att ggc tct agt ctg ttg att ctg gaa aat ctg gcc aac gat tca tat	576
Ile Gly Ser Ser Leu Leu Ile Leu Glu Asn Leu Ala Asn Asp Ser Tyr	
180 185 190	
ccg ccg att aca ttt tgt gtg gtc tct gga cat gtg aga cta ttg ata	624
Pro Pro Ile Thr Phe Cys Val Val Ser Gly His Val Arg Leu Leu Ile	
195 200 205	
atg cgt tta agt cga att ggt cac gat gta aaa tta tca agt tcg gaa	672
Met Arg Leu Ser Arg Ile Gly His Asp Val Lys Leu Ser Ser Ser Glu	
210 215 220	
aat acc aga aaa ctc atc gaa ggt atc cag gat cac agg aaa cta atg	720
Asn Thr Arg Lys Leu Ile Glu Gly Ile Gln Asp His Arg Lys Leu Met	
225 230 235 240	
aag ata ata cgc cta ctt cgc agc act tta cat ctt agc caa ctg ggc	768
Lys Ile Ile Arg Leu Leu Arg Ser Thr Leu His Leu Ser Gln Leu Gly	
245 250 255	
cag ttc ctt tct agt gga atc aac att tcc ata aca ctc atc aac atc	816
Gln Phe Leu Ser Ser Gly Ile Asn Ile Ser Ile Thr Leu Ile Asn Ile	
260 265 270	
ctg ttc ttt gcg gaa aac aac ttt gca atg ctt tat tat gcg gtg ttc	864
Leu Phe Phe Ala Glu Asn Asn Phe Ala Met Leu Tyr Tyr Ala Val Phe	
275 280 285	
ttt gct gca atg tta ata gaa cta ttt cca agt tgt tac tat gga att	912
Phe Ala Ala Met Leu Ile Glu Leu Phe Pro Ser Cys Tyr Tyr Gly Ile	
290 295 300	

ctg atg aca atg gag ttt gat aag cta cca tat gcc atc ttc tcc agc 960
 Leu Met Thr Met Glu Phe Asp Lys Leu Pro Tyr Ala Ile Phe Ser Ser
 305 310 315 320

aac tgg ctt aaa atg gat aaa aga tac aat cga tcc ttg ata att ctg 1008
 Asn Trp Leu Lys Met Asp Lys Arg Tyr Asn Arg Ser Leu Ile Ile Leu
 325 330 335

atg caa cta aca ctg gtt cca gtg aat ata aaa gca ggt ggt att gtt 1056
 Met Gln Leu Thr Leu Val Pro Val Asn Ile Lys Ala Gly Gly Ile Val
 340 345 350

ggc atc gat atg agt gca ttt ttt gcc aca gtt cgg atg gca tat tcc 1104
 Gly Ile Asp Met Ser Ala Phe Phe Ala Thr Val Arg Met Ala Tyr Ser
 355 360 365

ttt tac act tta gcc ttg tca ttt cga gta tag 1137
 Phe Tyr Thr Leu Ala Leu Ser Phe Arg Val
 370 375

<210> 12

<211> 378

<212> PRT

<213> Drosophila melanogaster

<400> 12

Met Asp Ser Arg Arg Lys Val Arg Ser Glu Asn Leu Tyr Lys Thr Tyr
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Trp Leu Tyr Trp Arg Leu Leu Gly Val Glu Gly Asp Tyr Pro Phe Arg
 20 25 30

Arg Leu Val Asp Phe Thr Ile Thr Ser Phe Ile Thr Ile Leu Phe Pro
 35 40 45

Val His Leu Ile Leu Gly Met Tyr Lys Lys Pro Gln Ile Gln Val Phe
 50 55 60

Arg Ser Leu His Phe Thr Ser Glu Cys Leu Phe Cys Ser Tyr Lys Phe
 65 70 75 80

Phe Cys Phe Arg Trp Lys Leu Lys Glu Ile Lys Thr Ile Glu Gly Leu
 85 90 95

Leu Gln Asp Leu Asp Ser Arg Val Glu Ser Glu Glu Glu Arg Asn Tyr
 100 105 110

Phe Asn Gln Asn Pro Ser Arg Val Ala Arg Met Leu Ser Lys Ser Tyr
115 120 125
Leu Val Ala Ala Ile Ser Ala Ile Ile Thr Ala Thr Val Ala Gly Leu
130 135 140
Phe Ser Thr Gly Arg Asn Leu Met Tyr Leu Gly Trp Phe Pro Tyr Asp
145 150 155 160
Phe Gln Ala Thr Ala Ala Ile Tyr Trp Ile Ser Phe Ser Tyr Gln Ala
165 170 175
Ile Gly Ser Ser Leu Leu Ile Leu Glu Asn Leu Ala Asn Asp Ser Tyr
180 185 190
Pro Pro Ile Thr Phe Cys Val Val Ser Gly His Val Arg Leu Leu Ile
195 200 205
Met Arg Leu Ser Arg Ile Gly His Asp Val Lys Leu Ser Ser Ser Glu
210 215 220
Asn Thr Arg Lys Leu Ile Glu Gly Ile Gln Asp His Arg Lys Leu Met
225 230 235 240
Lys Ile Ile Arg Leu Leu Arg Ser Thr Leu His Leu Ser Gln Leu Gly
245 250 255
Gln Phe Leu Ser Ser Gly Ile Asn Ile Ser Ile Thr Leu Ile Asn Ile
260 265 270
Leu Phe Phe Ala Glu Asn Asn Phe Ala Met Leu Tyr Tyr Ala Val Phe
275 280 285
Phe Ala Ala Met Leu Ile Glu Leu Phe Pro Ser Cys Tyr Tyr Gly Ile
290 295 300
Leu Met Thr Met Glu Phe Asp Lys Leu Pro Tyr Ala Ile Phe Ser Ser
305 310 315 320
Asn Trp Leu Lys Met Asp Lys Arg Tyr Asn Arg Ser Leu Ile Ile Leu
325 330 335
Met Gln Leu Thr Leu Val Pro Val Asn Ile Lys Ala Gly Gly Ile Val
340 345 350
Gly Ile Asp Met Ser Ala Phe Phe Ala Thr Val Arg Met Ala Tyr Ser
355 360 365

Phe Tyr Thr Leu Ala Leu Ser Phe Arg Val
 370 375

<210> 13
 <211> 1140
 <212> DNA
 <213> Drosophila melanogaster

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 <222> (1)..(1137)
 <223> DOR 33B.2, a coding region on BDGP Clone No.
 AC006240

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 Tyr Trp Leu Tyr Trp His Leu Leu Gly Leu Glu Ser Asn Phe Phe Leu
 20 25 30
 aat cgc ttg ttg gat ttg gtg att aca att ttc gta acc att tgg tat 144
 Asn Arg Leu Leu Asp Leu Val Ile Thr Ile Phe Val Thr Ile Trp Tyr
 35 40 45
 cca att cac ctg att ctg gga ctg ttt atg gaa aga tct ttg ggg gat 192
 Pro Ile His Leu Ile Leu Gly Leu Phe Met Glu Arg Ser Leu Gly Asp
 50 55 60
 gtc tgc aag ggt cta cca att acg gca gca tgc ttt ttc gcc agc ttt 240
 Val Cys Lys Gly Leu Pro Ile Thr Ala Ala Cys Phe Phe Ala Ser Phe
 65 70 75 80
 aaa ttt att tgt ttt cgc ttc aag cta tct gaa att aaa gaa atc gaa 288
 Lys Phe Ile Cys Phe Arg Phe Lys Leu Ser Glu Ile Lys Glu Ile Glu
 85 90 95
 ata tta ttt aaa gag ctg gat cag cga gct tta agt cga gag gaa tgc 336
 Ile Leu Phe Lys Glu Leu Asp Gln Arg Ala Leu Ser Arg Glu Glu Cys
 100 105 110
 gag ttt ttc aat caa aat acg aga cgt gag gcg aat ttc att tgg aaa 384
 Glu Phe Phe Asn Gln Asn Thr Arg Arg Glu Ala Asn Phe Ile Trp Lys
 115 120 125

agt ttc att gtg gcc tat gga ctg tcg aat atc tcg gct att gca tca	432
Ser Phe Ile Val Ala Tyr Gly Leu Ser Asn Ile Ser Ala Ile Ala Ser	
130 135 140	
gtt ctt ttc ggc ggt gga cat aag cta tta tat ccc gcc tgg ttt cca	480
Val Leu Phe Gly Gly Gly His Lys Leu Leu Tyr Pro Ala Trp Phe Pro	
145 150 155 160	
tac gat gtg cag gcc acg gaa cta ata ttt tgg cta agt gta aca tac	528
Tyr Asp Val Gln Ala Thr Glu Leu Ile Phe Trp Leu Ser Val Thr Tyr	
165 170 175	
caa att gcc gga gta agt ttg gcc ata ctt cag aat ttg gcc aat gat	576
Gln Ile Ala Gly Val Ser Leu Ala Ile Leu Gln Asn Leu Ala Asn Asp	
180 185 190	
tcc tat cca ccg atg aca ttt tgc gtg gtt gcc ggt cat gta aga ctt	624
Ser Tyr Pro Pro Met Thr Phe Cys Val Val Ala Gly His Val Arg Leu	
195 200 205	
ttg gcg atg cgc ttg agt aga att ggc caa ggt cca gag gaa aca ata	672
Leu Ala Met Arg Leu Ser Arg Ile Gly Gln Gly Pro Glu Glu Thr Ile	
210 215 220	
tac tta acc gga aag caa tta atc gaa agc atc gag gat cac cga aaa	720
Tyr Leu Thr Gly Lys Gln Leu Ile Glu Ser Ile Glu Asp His Arg Lys	
225 230 235 240	
cta atg aaa ata gtg gaa tta ctg cgc agc acc atg aat att tcg cag	768
Leu Met Lys Ile Val Glu Leu Leu Arg Ser Thr Met Asn Ile Ser Gln	
245 250 255	
ctc ggc cag ttt att tca agt ggt gtt aat att tcc ata aca cta gtc	816
Leu Gly Gln Phe Ile Ser Ser Gly Val Asn Ile Ser Ile Thr Leu Val	
260 265 270	
aac att ctc ttc ttt gcg gat aat aat ttc gct ata acc tac tac gga	864
Asn Ile Leu Phe Phe Ala Asp Asn Asn Phe Ala Ile Thr Tyr Tyr Gly	
275 280 285	
gtg tac ttc cta tcg atg gtg ttg gaa tta ttc ccg tgc tgc tat tac	912
Val Tyr Phe Leu Ser Met Val Leu Glu Leu Phe Pro Cys Cys Tyr Tyr	
290 295 300	
ggc acc ctg ata tcc gtg gag atg aac cag ctg acc tat gcg att tac	960
Gly Thr Leu Ile Ser Val Glu Met Asn Gln Leu Thr Tyr Ala Ile Tyr	
305 310 315 320	

tca agt aac tgg atg agt atg aat cgg agc tac agc cgc atc cta ctg 1008
 Ser Ser Asn Trp Met Ser Met Asn Arg Ser Tyr Ser Arg Ile Leu Leu
 325 330 335

atc ttc atg caa ctc acc ctg gcg gaa gtg cag atc aag gcc ggt ggg 1056
 Ile Phe Met Gln Leu Thr Leu Ala Glu Val Gln Ile Lys Ala Gly Gly
 340 345 350

atg att ggc atc gga atg aac gcc ttc ttt gcc acc gtg cga ttg gcc 1104
 Met Ile Gly Ile Gly Met Asn Ala Phe Phe Ala Thr Val Arg Leu Ala
 355 360 365

tac tcc ttc ttc act ttg gcc atg tcg ctg cgt taa 1140
 Tyr Ser Phe Phe Thr Leu Ala Met Ser Leu Arg
 370 375

<210> 14
 <211> 379
 <212> PRT
 <213> Drosophila melanogaster

<400> 14
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Tyr Trp Leu Tyr Trp His Leu Leu Gly Leu Glu Ser Asn Phe Phe Leu
 20 25 30

Asn Arg Leu Leu Asp Leu Val Ile Thr Ile Phe Val Thr Ile Trp Tyr
 35 40 45

Pro Ile His Leu Ile Leu Gly Leu Phe Met Glu Arg Ser Leu Gly Asp
 50 55 60

Val Cys Lys Gly Leu Pro Ile Thr Ala Ala Cys Phe Phe Ala Ser Phe
 65 70 75 80

Lys Phe Ile Cys Phe Arg Phe Lys Leu Ser Glu Ile Lys Glu Ile Glu
 85 90 95

Ile Leu Phe Lys Glu Leu Asp Gln Arg Ala Leu Ser Arg Glu Glu Cys
 100 105 110

Glu Phe Phe Asn Gln Asn Thr Arg Arg Glu Ala Asn Phe Ile Trp Lys
 115 120 125

Ser Phe Ile Val Ala Tyr Gly Leu Ser Asn Ile Ser Ala Ile Ala Ser
 130 135 140

Val Leu Phe Gly Gly Gly His Lys Leu Leu Tyr Pro Ala Trp Phe Pro
 145 150 155 160

Tyr Asp Val Gln Ala Thr Glu Leu Ile Phe Trp Leu Ser Val Thr Tyr
 165 170 175

Gln Ile Ala Gly Val Ser Leu Ala Ile Leu Gln Asn Leu Ala Asn Asp
 180 185 190

Ser Tyr Pro Pro Met Thr Phe Cys Val Val Ala Gly His Val Arg Leu
 195 200 205

Leu Ala Met Arg Leu Ser Arg Ile Gly Gln Gly Pro Glu Glu Thr Ile
 210 215 220

Tyr Leu Thr Gly Lys Gln Leu Ile Glu Ser Ile Glu Asp His Arg Lys
 225 230 235 240

Leu Met Lys Ile Val Glu Leu Leu Arg Ser Thr Met Asn Ile Ser Gln
 245 250 255

Leu Gly Gln Phe Ile Ser Ser Gly Val Asn Ile Ser Ile Thr Leu Val
 260 265 270

Asn Ile Leu Phe Phe Ala Asp Asn Asn Phe Ala Ile Thr Tyr Tyr Gly
 275 280 285

Val Tyr Phe Leu Ser Met Val Leu Glu Leu Phe Pro Cys Cys Tyr Tyr
 290 295 300

Gly Thr Leu Ile Ser Val Glu Met Asn Gln Leu Thr Tyr Ala Ile Tyr
 305 310 315 320

Ser Ser Asn Trp Met Ser Met Asn Arg Ser Tyr Ser Arg Ile Leu Leu
 325 330 335

Ile Phe Met Gln Leu Thr Leu Ala Glu Val Gln Ile Lys Ala Gly Gly
 340 345 350

Met Ile Gly Ile Gly Met Asn Ala Phe Phe Ala Thr Val Arg Leu Ala
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Tyr Ser Phe Phe Thr Leu Ala Met Ser Leu Arg
 370 375

<210> 15
 <211> 1155
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
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 <222> (1)..(1152)
 <223> DOR 33B3.3, a coding region on BDGP Clone No.
 AC006240

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atg cga ttg ctg gta ccg act ttc ttc aag gat tcc tca cgt cct gtc 96
 Met Arg Leu Leu Val Pro Thr Phe Phe Lys Asp Ser Ser Arg Pro Val
 20 25 30

cag ctg tac gtg gtg ttg ctg cac atc ctg gtc acc ttg tgg ttt cca 144
 Gln Leu Tyr Val Val Leu Leu His Ile Leu Val Thr Leu Trp Phe Pro
 35 40 45

ctg cat ctg ctg ctg cat ctt ctg cta ctt cca tct acc gct gag ttc 192
 Leu His Leu Leu Leu His Leu Leu Leu Leu Pro Ser Thr Ala Glu Phe
 50 55 60

ttt aag aac ctg acc atg tct ctg act tgt gtg gcc tgc agt ctg aag 240
 Phe Lys Asn Leu Thr Met Ser Leu Thr Cys Val Ala Cys Ser Leu Lys
 65 70 75 80

cat gtg gcc cac ttg tat cac ttg ccg cag att gtg gaa atc gaa tca 288
 His Val Ala His Leu Tyr His Leu Pro Gln Ile Val Glu Ile Glu Ser
 85 90 95

ctg atc gag caa tta gac aca ttt att gcc agc gaa cag gag cat cgt 336
 Leu Ile Glu Gln Leu Asp Thr Phe Ile Ala Ser Glu Gln Glu His Arg
 100 105 110

tac tat cgg gat cac gta cat tgc cat gct agg cgc ttt aca aga tgt 384
 Tyr Tyr Arg Asp His Val His Cys His Ala Arg Arg Phe Thr Arg Cys
 115 120 125

ctc tat att agc ttt ggc atg atc tat gcg ctt ttc ctg ttc ggc gtc 432
 Leu Tyr Ile Ser Phe Gly Met Ile Tyr Ala Leu Phe Leu Phe Gly Val

130	135	140	
ttc gtt cag gtt att agc gga aat tgg gaa ctt ctc tat cca gcc tat			480
Phe Val Gln Val Ile Ser Gly Asn Trp Glu Leu Leu Tyr Pro Ala Tyr			
145	150	155	160
ttc cca ttc gac ttg gag agc aat cgc ttt ctc ggc gca gta gcc ttg			528
Phe Pro Phe Asp Leu Glu Ser Asn Arg Phe Leu Gly Ala Val Ala Leu			
	165	170	175
ggc tat cag gta ttc agc atg tta gtt gaa ggc ttc cag ggg ctg ggc			576
Gly Tyr Gln Val Phe Ser Met Leu Val Glu Gly Phe Gln Gly Leu Gly			
	180	185	190
aac gat acc tat acc cca ctg acc cta tgc ctt ctg gcc gga cat gtc			624
Asn Asp Thr Tyr Thr Pro Leu Thr Leu Cys Leu Leu Ala Gly His Val			
	195	200	205
cat ttg tgg tcc ata cga atg ggt caa ctg gga tac ttc gat gac gag			672
His Leu Trp Ser Ile Arg Met Gly Gln Leu Gly Tyr Phe Asp Asp Glu			
	210	215	220
acg gtg gtg aat cat cag cgt ttg ctg gat tac att gag cag cat aaa			720
Thr Val Val Asn His Gln Arg Leu Leu Asp Tyr Ile Glu Gln His Lys			
	225	230	235
ctc ttg gtg cga ttc cac aac ctg gtg agc cgg acc atc agc gaa gtg			768
Leu Leu Val Arg Phe His Asn Leu Val Ser Arg Thr Ile Ser Glu Val			
	245	250	255
caa ctg gtg cag ctg ggc gga tgt gga gcc act ctg tgc atc att gtc			816
Gln Leu Val Gln Leu Gly Gly Cys Gly Ala Thr Leu Cys Ile Ile Val			
	260	265	270
tcc tac atg ctc ttc ttt gtg ggc gac aca atc tcg ctg gtc tac tac			864
Ser Tyr Met Leu Phe Phe Val Gly Asp Thr Ile Ser Leu Val Tyr Tyr			
	275	280	285
ttg gtg ttc ttt gga gtg gtc tgc gtg cag ctc ttt ccc agc tgc tat			912
Leu Val Phe Phe Gly Val Val Cys Val Gln Leu Phe Pro Ser Cys Tyr			
	290	295	300
ttt gcc agc gaa gta gcc gag gag ttg gaa cgg ctg cca tat gcg atc			960
Phe Ala Ser Glu Val Ala Glu Glu Leu Glu Arg Leu Pro Tyr Ala Ile			
	305	310	315
ttc tcc agc aga tgg tac gat caa tcg cgg gat cat cga ttc gat ttg			1008
Phe Ser Ser Arg Trp Tyr Asp Gln Ser Arg Asp His Arg Phe Asp Leu			

[illegible]

	130						135							140		
Phe	Val	Gln	Val	Ile	Ser	Gly	Asn	Trp	Glu	Leu	Leu	Tyr	Pro	Ala	Tyr	
145					150					155						160
Phe	Pro	Phe	Asp	Leu	Glu	Ser	Asn	Arg	Phe	Leu	Gly	Ala	Val	Ala	Leu	
				165					170					175		
Gly	Tyr	Gln	Val	Phe	Ser	Met	Leu	Val	Glu	Gly	Phe	Gln	Gly	Leu	Gly	
			180					185					190			
Asn	Asp	Thr	Tyr	Thr	Pro	Leu	Thr	Leu	Cys	Leu	Leu	Ala	Gly	His	Val	
		195					200					205				
His	Leu	Trp	Ser	Ile	Arg	Met	Gly	Gln	Leu	Gly	Tyr	Phe	Asp	Asp	Glu	
	210					215					220					
Thr	Val	Val	Asn	His	Gln	Arg	Leu	Leu	Asp	Tyr	Ile	Glu	Gln	His	Lys	
225					230					235					240	
Leu	Leu	Val	Arg	Phe	His	Asn	Leu	Val	Ser	Arg	Thr	Ile	Ser	Glu	Val	
				245					250					255		
Gln	Leu	Val	Gln	Leu	Gly	Gly	Cys	Gly	Ala	Thr	Leu	Cys	Ile	Ile	Val	
			260					265					270			
Ser	Tyr	Met	Leu	Phe	Phe	Val	Gly	Asp	Thr	Ile	Ser	Leu	Val	Tyr	Tyr	
		275					280					285				
Leu	Val	Phe	Phe	Gly	Val	Val	Cys	Val	Gln	Leu	Phe	Pro	Ser	Cys	Tyr	
	290					295					300					
Phe	Ala	Ser	Glu	Val	Ala	Glu	Glu	Leu	Glu	Arg	Leu	Pro	Tyr	Ala	Ile	
305					310					315					320	
Phe	Ser	Ser	Arg	Trp	Tyr	Asp	Gln	Ser	Arg	Asp	His	Arg	Phe	Asp	Leu	
				325					330					335		
Leu	Ile	Phe	Thr	Gln	Leu	Thr	Leu	Gly	Asn	Arg	Gly	Trp	Ile	Ile	Lys	
			340					345					350			
Ala	Gly	Gly	Leu	Ile	Glu	Leu	Asn	Leu	Asn	Ala	Phe	Phe	Ala	Thr	Leu	
		355					360					365				
Lys	Met	Ala	Tyr	Ser	Leu	Phe	Ala	Val	Val	Val	Arg	Ala	Lys	Gly	Ile	
	370					375					380					

<210> 17
 <211> 1152
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(1149)
 <223> DOR 43B.1, coding region of AF127926

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 cga cac ttg gcc gtg ctg tac ccc act ccg ggc tcc agc tgg cgc aag 96
 Arg His Leu Ala Val Leu Tyr Pro Thr Pro Gly Ser Ser Trp Arg Lys
 20 25 30
 ttc gcc ttc gtg ctg ccg gtg act gcg atg aat ctg atg cag ttc gtc 144
 Phe Ala Phe Val Leu Pro Val Thr Ala Met Asn Leu Met Gln Phe Val
 35 40 45
 tac ctg ctg cgg atg tgg ggc gac ctg ccc gcc ttc att ctg aac atg 192
 Tyr Leu Leu Arg Met Trp Gly Asp Leu Pro Ala Phe Ile Leu Asn Met
 50 55 60
 ttc ttc ttc tcg gcc att ttc aac gcc ctg atg cgc acg tgg ctg gtc 240
 Phe Phe Phe Ser Ala Ile Phe Asn Ala Leu Met Arg Thr Trp Leu Val
 65 70 75 80
 ata atc aag cgg cgc cag ttc gag gag ttt ctc ggc caa ctg gcc act 288
 Ile Ile Lys Arg Arg Gln Phe Glu Glu Phe Leu Gly Gln Leu Ala Thr
 85 90 95
 ctg ttc cat tcg att ctc gac tcc acc gac gag tgg ggg cgt gcc atc 336
 Leu Phe His Ser Ile Leu Asp Ser Thr Asp Glu Trp Gly Arg Gly Ile
 100 105 110
 ctg cgg agg gcg gaa cgg gag gct cgg aac ctg gcc atc ctt aat ttg 384
 Leu Arg Arg Ala Glu Arg Glu Ala Arg Asn Leu Ala Ile Leu Asn Leu
 115 120 125
 agt gcc tcc ttc ctg gac att gtc ggt gct ctg ttt ttc gaa tat aaa 432
 Ser Ala Ser Phe Leu Asp Ile Val Gly Ala Leu Phe Phe Glu Tyr Lys
 130 135 140

ttc cca att ggt gtt gtc act ttt ttc ctt cca gct cat ccc ttc ggc	480
Phe Pro Ile Gly Val Val Thr Phe Phe Leu Pro Ala His Pro Phe Gly	
145 150 155 160	
tta gct cta cca gga gtg agc atg acc agt tca ccc gtc tac gag gtt	528
Leu Ala Leu Pro Gly Val Ser Met Thr Ser Ser Pro Val Tyr Glu Val	
165 170 175	
atc tac ttg gcc caa ctg cct acg ccc ctg ctg ctg tcc atg atg tac	576
Ile Tyr Leu Ala Gln Leu Pro Thr Pro Leu Leu Leu Ser Met Met Tyr	
180 185 190	
atg cct ttc gtc agc ctt ttt gcc ggc ctg gcc atc ttt ggg aag gcc	624
Met Pro Phe Val Ser Leu Phe Ala Gly Leu Ala Ile Phe Gly Lys Ala	
195 200 205	
atg ctg cag atc ctg gta cac agg ctg ggc cag att ggc gga gaa gag	672
Met Leu Gln Ile Leu Val His Arg Leu Gly Gln Ile Gly Gly Glu Glu	
210 215 220	
cag tcg gag gag gag cgc ttc caa agg ctg gcc tcc tgc att gcg tac	720
Gln Ser Glu Glu Glu Arg Phe Gln Arg Leu Ala Ser Cys Ile Ala Tyr	
225 230 235 240	
cac acg cag gtg atg cgc tat gtg tgg cag ctc aac aaa ctg gtg gcc	768
His Thr Gln Val Met Arg Tyr Val Trp Gln Leu Asn Lys Leu Val Ala	
245 250 255	
aac att gtg gcg gtg gaa gca att att ttt ggc tcg ata atc tgc tca	816
Asn Ile Val Ala Val Glu Ala Ile Ile Phe Gly Ser Ile Ile Cys Ser	
260 265 270	
ctg ctc ttc tgt ctg aat att ata acc tca ccc acc cag gtg atc tcg	864
Leu Leu Phe Cys Leu Asn Ile Ile Thr Ser Pro Thr Gln Val Ile Ser	
275 280 285	
ata gtg atg tac att ctg acc atg ctg tac gtt ctc ttc acc tac tac	912
Ile Val Met Tyr Ile Leu Thr Met Leu Tyr Val Leu Phe Thr Tyr Tyr	
290 295 300	
aat cgg gcc aat gaa ata tgc ctc gag aac aac cgg gtg gcg gag gct	960
Asn Arg Ala Asn Glu Ile Cys Leu Glu Asn Asn Arg Val Ala Glu Ala	
305 310 315 320	
gtt tac aat gtg ccc tgg tac gag gca gga act cgg ttt cgc aaa acc	1008
Val Tyr Asn Val Pro Trp Tyr Glu Ala Gly Thr Arg Phe Arg Lys Thr	
325 330 335	

ctc ctg atc ttc ttg atg caa aca caa cac ccg atg gag ata aga gtc 1056
 Leu Leu Ile Phe Leu Met Gln Thr Gln His Pro Met Glu Ile Arg Val
 340 345 350

ggc aac gtt tac ccc atg aca ttg gcc atg ttc cag agt ctg ttg aat 1104
 Gly Asn Val Tyr Pro Met Thr Leu Ala Met Phe Gln Ser Leu Leu Asn
 355 360 365

gcg tcc tac tcc tac ttt acc atg ctg cgt ggc gtc acc ggc aaa tga 1152
 Ala Ser Tyr Ser Tyr Phe Thr Met Leu Arg Gly Val Thr Gly Lys
 370 375 380

<210> 18

<211> 383

<212> PRT

<213> Drosophila melanogaster

<400> 18

Met Thr Ile Glu Asp Ile Gly Leu Val Gly Ile Asn Val Arg Met Trp
 1 5 10 15

Arg His Leu Ala Val Leu Tyr Pro Thr Pro Gly Ser Ser Trp Arg Lys
 20 25 30

Phe Ala Phe Val Leu Pro Val Thr Ala Met Asn Leu Met Gln Phe Val
 35 40 45

Tyr Leu Leu Arg Met Trp Gly Asp Leu Pro Ala Phe Ile Leu Asn Met
 50 55 60

Phe Phe Phe Ser Ala Ile Phe Asn Ala Leu Met Arg Thr Trp Leu Val
 65 70 75 80

Ile Ile Lys Arg Arg Gln Phe Glu Glu Phe Leu Gly Gln Leu Ala Thr
 85 90 95

Leu Phe His Ser Ile Leu Asp Ser Thr Asp Glu Trp Gly Arg Gly Ile
 100 105 110

Leu Arg Arg Ala Glu Arg Glu Ala Arg Asn Leu Ala Ile Leu Asn Leu
 115 120 125

Ser Ala Ser Phe Leu Asp Ile Val Gly Ala Leu Phe Phe Glu Tyr Lys
 130 135 140

Phe Pro Ile Gly Val Val Thr Phe Phe Leu Pro Ala His Pro Phe Gly
 145 150 155 160

Leu Ala Leu Pro Gly Val Ser Met Thr Ser Ser Pro Val Tyr Glu Val
165 170 175

Ile Tyr Leu Ala Gln Leu Pro Thr Pro Leu Leu Leu Ser Met Met Tyr
180 185 190

Met Pro Phe Val Ser Leu Phe Ala Gly Leu Ala Ile Phe Gly Lys Ala
195 200 205

Met Leu Gln Ile Leu Val His Arg Leu Gly Gln Ile Gly Gly Glu Glu
210 215 220

Gln Ser Glu Glu Glu Arg Phe Gln Arg Leu Ala Ser Cys Ile Ala Tyr
225 230 235 240

His Thr Gln Val Met Arg Tyr Val Trp Gln Leu Asn Lys Leu Val Ala
245 250 255

Asn Ile Val Ala Val Glu Ala Ile Ile Phe Gly Ser Ile Ile Cys Ser
260 265 270

Leu Leu Phe Cys Leu Asn Ile Ile Thr Ser Pro Thr Gln Val Ile Ser
275 280 285

Ile Val Met Tyr Ile Leu Thr Met Leu Tyr Val Leu Phe Thr Tyr Tyr
290 295 300

Asn Arg Ala Asn Glu Ile Cys Leu Glu Asn Asn Arg Val Ala Glu Ala
305 310 315 320

Val Tyr Asn Val Pro Trp Tyr Glu Ala Gly Thr Arg Phe Arg Lys Thr
325 330 335

Leu Leu Ile Phe Leu Met Gln Thr Gln His Pro Met Glu Ile Arg Val
340 345 350

Gly Asn Val Tyr Pro Met Thr Leu Ala Met Phe Gln Ser Leu Leu Asn
355 360 365

Ala Ser Tyr Ser Tyr Phe Thr Met Leu Arg Gly Val Thr Gly Lys
370 375 380

<210> 19

<211> 1158

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1155)

<223> DOR 46F.1, a coding region on BDGP Clone No.

AC005974

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aac atc ctc tcg ttg tgg cct cag ata gaa cgc cgg tgg aga atc atc	96
Asn Ile Leu Ser Leu Trp Pro Gln Ile Glu Arg Arg Trp Arg Ile Ile	
20 25 30	

cac cag gtg aac tat gtc cac gta att gtg ttt tgg gtg ctg ctc ttt	144
His Gln Val Asn Tyr Val His Val Ile Val Phe Trp Val Leu Leu Phe	
35 40 45	

gat ctc ctc ttg gtg ctc cat gtg atg gct aat ttg agc tac atg tcc	192
Asp Leu Leu Leu Val Leu His Val Met Ala Asn Leu Ser Tyr Met Ser	
50 55 60	

gag gtt gtg aaa gcc atc ttt atc ctg gcc acc agt gca ggg cac acc	240
Glu Val Val Lys Ala Ile Phe Ile Leu Ala Thr Ser Ala Gly His Thr	
65 70 75 80	

acc aag ctg ctg tcc ata aag gcg aac aat gtg cag atg gag gag ctc	288
Thr Lys Leu Leu Ser Ile Lys Ala Asn Asn Val Gln Met Glu Glu Leu	
85 90 95	

ttt agg aga ttg gat aac gaa gag ttc cgt cct aga ggc gcc aac gaa	336
Phe Arg Arg Leu Asp Asn Glu Glu Phe Arg Pro Arg Gly Ala Asn Glu	
100 105 110	

gag ttg atc ttt gca gca gcc tgt gaa aga agt agg aag ctt cgg gac	384
Glu Leu Ile Phe Ala Ala Ala Cys Glu Arg Ser Arg Lys Leu Arg Asp	
115 120 125	

ttc tat gga gcg ctt tcg ttt gcc gcc ttg agc atg att ctc ata ccc	432
Phe Tyr Gly Ala Leu Ser Phe Ala Ala Leu Ser Met Ile Leu Ile Pro	
130 135 140	

cag ttc gcc ttg gac tgg tcc cac ctt ccg ctc aaa aca tac aat ccg	480
Gln Phe Ala Leu Asp Trp Ser His Leu Pro Leu Lys Thr Tyr Asn Pro	
145 150 155 160	

ctt ggc gag aat acc ggc tca cct gct tat tgg ctc ctc tac tgc tat	528
Leu Gly Glu Asn Thr Gly Ser Pro Ala Tyr Trp Leu Leu Tyr Cys Tyr	
165 170 175	
cag tgt ctg gcc ttg tcc gta tcc tgc atc acc aac ata gga ttc gac	576
Gln Cys Leu Ala Leu Ser Val Ser Cys Ile Thr Asn Ile Gly Phe Asp	
180 185 190	
tca ctc tgc tcc tca ctg ttc atc ttc ctc aag tgc cag ctg gac att	624
Ser Leu Cys Ser Ser Leu Phe Ile Phe Leu Lys Cys Gln Leu Asp Ile	
195 200 205	
ctg gcc gtg cga ctg gac aag atc ggt cgg tta atc act act tct ggt	672
Leu Ala Val Arg Leu Asp Lys Ile Gly Arg Leu Ile Thr Thr Ser Gly	
210 215 220	
ggc act gtg gaa cag caa ctt aag gaa aat atc cgc tat cac atg acc	720
Gly Thr Val Glu Gln Gln Leu Lys Glu Asn Ile Arg Tyr His Met Thr	
225 230 235 240	
atc gtt gaa ctg tcg aaa acc gtg gag cgt cta ctt tgc aag ccg att	768
Ile Val Glu Leu Ser Lys Thr Val Glu Arg Leu Leu Cys Lys Pro Ile	
245 250 255	
tcg gtg cag atc ttc tgc tcg gtt ttg gtg ctg act gcc aat ttc tat	816
Ser Val Gln Ile Phe Cys Ser Val Leu Val Leu Thr Ala Asn Phe Tyr	
260 265 270	
gcc att gct gtg tta tct gac gag agg ctg gag ctc ttt aag tat gtg	864
Ala Ile Ala Val Leu Ser Asp Glu Arg Leu Glu Leu Phe Lys Tyr Val	
275 280 285	
acc tat cag gcg tgc atg ttg att cag att ttt ata ttg tgc tac tat	912
Thr Tyr Gln Ala Cys Met Leu Ile Gln Ile Phe Ile Leu Cys Tyr Tyr	
290 295 300	
gcc ggt gag gta acc cag cgc agc ctg gac ctt ccg cac gag ctg tac	960
Ala Gly Glu Val Thr Gln Arg Ser Leu Asp Leu Pro His Glu Leu Tyr	
305 310 315 320	
aag acc tcc tgg gtg gac tgg gac tac agg agc cga agg att gcg ctc	1008
Lys Thr Ser Trp Val Asp Trp Asp Tyr Arg Ser Arg Arg Ile Ala Leu	
325 330 335	
ctc ttt atg caa cgc ctt cac tcg acc ttg agg att agg aca ctt aat	1056
Leu Phe Met Gln Arg Leu His Ser Thr Leu Arg Ile Arg Thr Leu Asn	
340 345 350	

cca agt ctt ggt ttt gac tta atg ctc ttc agc tcg gtg agt tct ttc 1104
 Pro Ser Leu Gly Phe Asp Leu Met Leu Phe Ser Ser Val Ser Ser Phe
 355 360 365

cgt gtt ttg act ttt ttg tgc act gta gcc aat ttc cat aat gag gct 1152
 Arg Val Leu Thr Phe Leu Cys Thr Val Ala Asn Phe His Asn Glu Ala
 370 375 380

cat tag 1158
 His
 385

<210> 20

<211> 385

<212> PRT

<213> Drosophila melanogaster

<400> 20

Met Ser Lys Gly Val Glu Ile Phe Tyr Lys Gly Gln Lys Ala Phe Leu
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Asn Ile Leu Ser Leu Trp Pro Gln Ile Glu Arg Arg Trp Arg Ile Ile
 20 25 30

His Gln Val Asn Tyr Val His Val Ile Val Phe Trp Val Leu Leu Phe
 35 40 45

Asp Leu Leu Leu Val Leu His Val Met Ala Asn Leu Ser Tyr Met Ser
 50 55 60

Glu Val Val Lys Ala Ile Phe Ile Leu Ala Thr Ser Ala Gly His Thr
 65 70 75 80

Thr Lys Leu Leu Ser Ile Lys Ala Asn Asn Val Gln Met Glu Glu Leu
 85 90 95

Phe Arg Arg Leu Asp Asn Glu Glu Phe Arg Pro Arg Gly Ala Asn Glu
 100 105 110

Glu Leu Ile Phe Ala Ala Ala Cys Glu Arg Ser Arg Lys Leu Arg Asp
 115 120 125

Phe Tyr Gly Ala Leu Ser Phe Ala Ala Leu Ser Met Ile Leu Ile Pro
 130 135 140

Gln Phe Ala Leu Asp Trp Ser His Leu Pro Leu Lys Thr Tyr Asn Pro

145		150		155		160
Leu Gly Glu Asn Thr Gly Ser Pro Ala Tyr Trp Leu Leu Tyr Cys Tyr						
	165		170		175	
Gln Cys Leu Ala Leu Ser Val Ser Cys Ile Thr Asn Ile Gly Phe Asp						
	180		185		190	
Ser Leu Cys Ser Ser Leu Phe Ile Phe Leu Lys Cys Gln Leu Asp Ile						
	195		200		205	
Leu Ala Val Arg Leu Asp Lys Ile Gly Arg Leu Ile Thr Thr Ser Gly						
	210		215		220	
Gly Thr Val Glu Gln Gln Leu Lys Glu Asn Ile Arg Tyr His Met Thr						
225		230		235		240
Ile Val Glu Leu Ser Lys Thr Val Glu Arg Leu Leu Cys Lys Pro Ile						
	245		250		255	
Ser Val Gln Ile Phe Cys Ser Val Leu Val Leu Thr Ala Asn Phe Tyr						
	260		265		270	
Ala Ile Ala Val Leu Ser Asp Glu Arg Leu Glu Leu Phe Lys Tyr Val						
	275		280		285	
Thr Tyr Gln Ala Cys Met Leu Ile Gln Ile Phe Ile Leu Cys Tyr Tyr						
290		295		300		
Ala Gly Glu Val Thr Gln Arg Ser Leu Asp Leu Pro His Glu Leu Tyr						
305		310		315		320
Lys Thr Ser Trp Val Asp Trp Asp Tyr Arg Ser Arg Arg Ile Ala Leu						
	325		330		335	
Leu Phe Met Gln Arg Leu His Ser Thr Leu Arg Ile Arg Thr Leu Asn						
	340		345		350	
Pro Ser Leu Gly Phe Asp Leu Met Leu Phe Ser Ser Val Ser Ser Phe						
	355		360		365	
Arg Val Leu Thr Phe Leu Cys Thr Val Ala Asn Phe His Asn Glu Ala						
	370		375		380	
His						
385						

<210> 21
 <211> 1155
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(1152)
 <223> DOR 46F.2, a coding region on BDGP Clone No.
 AC005974

<400> 21
 atg gtt acg gag gac ttt tat aag tac cag gtg tgg tac ttc caa atc 48
 Met Val Thr Glu Asp Phe Tyr Lys Tyr Gln Val Trp Tyr Phe Gln Ile
 1 5 10 15
 ctt ggt gtt tgg cag ctc ccc act tgg gcc gca gac cac cag cgt cgt 96
 Leu Gly Val Trp Gln Leu Pro Thr Trp Ala Ala Asp His Gln Arg Arg
 20 25 30
 ttt cag tcc atg agg ttt ggc ttc atc ctg gtc atc ctg ttc atc atg 144
 Phe Gln Ser Met Arg Phe Gly Phe Ile Leu Val Ile Leu Phe Ile Met
 35 40 45
 ctg ctg ctt ttc tcc ttc gaa atg ttg aac aac att tcc caa gtt agg 192
 Leu Leu Leu Phe Ser Phe Glu Met Leu Asn Asn Ile Ser Gln Val Arg
 50 55 60
 gag atc cta aag gta ttc ttc atg ttc gcc acg gaa ata tcc tgc atg 240
 Glu Ile Leu Lys Val Phe Phe Met Phe Ala Thr Glu Ile Ser Cys Met
 65 70 75 80
 gcc aaa tta ttg cat ttg aag ttg aag agc cgc aaa ctc gct ggc ttg 288
 Ala Lys Leu Leu His Leu Lys Leu Lys Ser Arg Lys Leu Ala Gly Leu
 85 90 95
 gtt gat gcg atg ttg tcc cca gag ttc ggc gtt aaa agt gaa cag gaa 336
 Val Asp Ala Met Leu Ser Pro Glu Phe Gly Val Lys Ser Glu Gln Glu
 100 105 110
 atg cag atg ctg gaa ttg gat aga gtg gcg gtt gtc cgc atg agg aac 384
 Met Gln Met Leu Glu Leu Asp Arg Val Ala Val Val Arg Met Arg Asn
 115 120 125
 tcc tac ggc atc atg tcc ctg ggc gcg gct tcc ctg atc ctt ata gtt 432
 Ser Tyr Gly Ile Met Ser Leu Gly Ala Ala Ser Leu Ile Leu Ile Val
 130 135 140

att gtc ctt ctc atg atg cag cgc ttt aat tcc ccg atg ctc ctg agc 1056
 Ile Val Leu Leu Met Met Gln Arg Phe Asn Ser Pro Met Leu Leu Ser
 340 345 350

acc ttt aac ccc acc ttt gct ttc agc ttg gag gcc ttt ggt tct atc 1104
 Thr Phe Asn Pro Thr Phe Ala Phe Ser Leu Glu Ala Phe Gly Ser Ile
 355 360 365

gtc aac tgc tcc tac agc tac ttc gca ctg ctg aag cgc gtc aac agt 1152
 Val Asn Cys Ser Tyr Ser Tyr Phe Ala Leu Leu Lys Arg Val Asn Ser
 370 375 380

taa 1155

<210> 22

<211> 384

<212> PRT

<213> Drosophila melanogaster

<400> 22

Met Val Thr Glu Asp Phe Tyr Lys Tyr Gln Val Trp Tyr Phe Gln Ile
 1 5 10 15

Leu Gly Val Trp Gln Leu Pro Thr Trp Ala Ala Asp His Gln Arg Arg
 20 25 30

Phe Gln Ser Met Arg Phe Gly Phe Ile Leu Val Ile Leu Phe Ile Met
 35 40 45

Leu Leu Leu Phe Ser Phe Glu Met Leu Asn Asn Ile Ser Gln Val Arg
 50 55 60

Glu Ile Leu Lys Val Phe Phe Met Phe Ala Thr Glu Ile Ser Cys Met
 65 70 75 80

Ala Lys Leu Leu His Leu Lys Leu Lys Ser Arg Lys Leu Ala Gly Leu
 85 90 95

Val Asp Ala Met Leu Ser Pro Glu Phe Gly Val Lys Ser Glu Gln Glu
 100 105 110

Met Gln Met Leu Glu Leu Asp Arg Val Ala Val Val Arg Met Arg Asn
 115 120 125

Ser Tyr Gly Ile Met Ser Leu Gly Ala Ala Ser Leu Ile Leu Ile Val
 130 135 140

Pro Cys Phe Asp Asn Phe Gly Glu Leu Pro Leu Ala Met Leu Glu Val			
145	150	155	160
Cys Ser Ile Glu Gly Trp Ile Cys Tyr Trp Ser Gln Tyr Leu Phe His			
	165	170	175
Ser Ile Cys Leu Leu Pro Thr Cys Val Leu Asn Ile Thr Tyr Asp Ser			
	180	185	190
Val Ala Tyr Ser Leu Leu Cys Phe Leu Lys Val Gln Leu Gln Met Leu			
	195	200	205
Val Leu Arg Leu Glu Lys Leu Gly Pro Val Ile Glu Pro Gln Asp Asn			
	210	215	220
Glu Lys Ile Ala Met Glu Leu Arg Glu Cys Ala Ala Tyr Tyr Asn Arg			
225	230	235	240
Ile Val Arg Phe Lys Asp Leu Val Glu Leu Phe Ile Lys Gly Pro Gly			
	245	250	255
Ser Val Gln Leu Met Cys Ser Val Leu Val Leu Val Ser Asn Leu Tyr			
	260	265	270
Asp Met Ser Thr Met Ser Ile Ala Asn Gly Asp Ala Ile Phe Met Leu			
	275	280	285
Lys Thr Cys Ile Tyr Gln Leu Val Met Leu Trp Gln Ile Phe Ile Ile			
	290	295	300
Cys Tyr Ala Ser Asn Glu Val Thr Val Gln Ser Ser Arg Leu Cys His			
305	310	315	320
Ser Ile Tyr Ser Ser Gln Trp Thr Gly Trp Asn Arg Ala Asn Arg Arg			
	325	330	335
Ile Val Leu Leu Met Met Gln Arg Phe Asn Ser Pro Met Leu Leu Ser			
	340	345	350
Thr Phe Asn Pro Thr Phe Ala Phe Ser Leu Glu Ala Phe Gly Ser Ile			
	355	360	365
Val Asn Cys Ser Tyr Ser Tyr Phe Ala Leu Leu Lys Arg Val Asn Ser			
	370	375	380

<210> 23
 <211> 1158
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(1155)
 <223> DOR 47E.1, coding region of AF156880

<400> 23
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 Met Asp Ser Phe Leu Gln Val Gln Lys Ser Thr Ile Ala Leu Leu Gly
 1 5 10 15
 ttt gat ctc ttt agt gaa aat cga gaa atg tgg aaa cgc ccc tat aga 96
 Phe Asp Leu Phe Ser Glu Asn Arg Glu Met Trp Lys Arg Pro Tyr Arg
 20 25 30
 gca atg aat gtg ttt agc ata gct gcc att ttt ccc ttt atc ctg gca 144
 Ala Met Asn Val Phe Ser Ile Ala Ala Ile Phe Pro Phe Ile Leu Ala
 35 40 45
 gct gtg ctc cat aat tgg aag aat gta ttg ctg ctg gcc gat gcc atg 192
 Ala Val Leu His Asn Trp Lys Asn Val Leu Leu Leu Ala Asp Ala Met
 50 55 60
 gtg gcc cta cta ata acc att ctg ggc cta ttc aag ttt agc atg ata 240
 Val Ala Leu Leu Ile Thr Ile Leu Gly Leu Phe Lys Phe Ser Met Ile
 65 70 75 80
 ctt tac tta cgt cgc gat ttc aag cga ctg att gac aaa ttt cgt ttg 288
 Leu Tyr Leu Arg Arg Asp Phe Lys Arg Leu Ile Asp Lys Phe Arg Leu
 85 90 95
 ctc atg tcg aat gag gcg gaa cag gcc gag gaa tac gcc gag att ctc 336
 Leu Met Ser Asn Glu Ala Glu Gln Gly Glu Glu Tyr Ala Glu Ile Leu
 100 105 110
 aac gca gca aac aag cag gat caa cga atg tgc act ctg ttt agg act 384
 Asn Ala Ala Asn Lys Gln Asp Gln Arg Met Cys Thr Leu Phe Arg Thr
 115 120 125
 tgt ttc ctc ctc gcc tgg gcc ttg aat agt gtt ctg ccc ctc gtg aga 432
 Cys Phe Leu Leu Ala Trp Ala Leu Asn Ser Val Leu Pro Leu Val Arg
 130 135 140
 atg ggt ctc agc tat tgg tta gca ggt cat gca gag ccc gag ttg cct 480

Met Gly Leu Ser Tyr Trp Leu Ala Gly His Ala Glu Pro Glu Leu Pro	
145	150 155 160
ttt ccc tgt ctt ttt ccc tgg aat atc cac atc att cgc aat tat gtt	528
Phe Pro Cys Leu Phe Pro Trp Asn Ile His Ile Ile Arg Asn Tyr Val	
165 170 175	
ttg agc ttc atc tgg agc gct ttc gcc tcg aca ggt gtg gtt tta cct	576
Leu Ser Phe Ile Trp Ser Ala Phe Ala Ser Thr Gly Val Val Leu Pro	
180 185 190	
gct gtc agc ttg gat acc ata ttc tgt tcc ttc acc agc aac ctg tgc	624
Ala Val Ser Leu Asp Thr Ile Phe Cys Ser Phe Thr Ser Asn Leu Cys	
195 200 205	
gcc ttc ttc aaa att gcg cag tac aag gtg gtt aga ttt aag ggc gga	672
Ala Phe Phe Lys Ile Ala Gln Tyr Lys Val Val Arg Phe Lys Gly Gly	
210 215 220	
tcc ctt aaa gaa tca cag gcc aca ttg aac aaa gtc ttt gcc ctg tac	720
Ser Leu Lys Glu Ser Gln Ala Thr Leu Asn Lys Val Phe Ala Leu Tyr	
225 230 235 240	
cag acc agc ttg gat atg tgc aac gat ctg aat cag tgc tac caa ccg	768
Gln Thr Ser Leu Asp Met Cys Asn Asp Leu Asn Gln Cys Tyr Gln Pro	
245 250 255	
att atc tgc gcc cag ttc ttc att tca tct ctg caa ctc tgc atg ctg	816
Ile Ile Cys Ala Gln Phe Phe Ile Ser Ser Leu Gln Leu Cys Met Leu	
260 265 270	
gga tat ctg ttc tcc att act ttt gcc cag aca gag ggc gtc tac tat	864
Gly Tyr Leu Phe Ser Ile Thr Phe Ala Gln Thr Glu Gly Val Tyr Tyr	
275 280 285	
gcc tca ttc ata gcc aca atc att ata caa gcc tat atc tac tgc tac	912
Ala Ser Phe Ile Ala Thr Ile Ile Ile Gln Ala Tyr Ile Tyr Cys Tyr	
290 295 300	
tgc ggg gag aac ctg aag acg gag agt gcc agc ttc gag tgg gcc atc	960
Cys Gly Glu Asn Leu Lys Thr Glu Ser Ala Ser Phe Glu Trp Ala Ile	
305 310 315 320	
tac gac agt ccg tgg cac gag agt ttg ggt gct ggt gga gcc tct acc	1008
Tyr Asp Ser Pro Trp His Glu Ser Leu Gly Ala Gly Gly Ala Ser Thr	
325 330 335	
tcg atc tgc cga tcc ttg ctg atc agc atg atg cgg gct cat cgg gga	1056

Ser Ile Cys Arg Ser Leu Leu Ile Ser Met Met Arg Ala His Arg Gly
340 345 350

ttc cgc att acg gga tac ttt ttc gag gca aac atg gag gcc ttc tca 1104
Phe Arg Ile Thr Gly Tyr Phe Phe Glu Ala Asn Met Glu Ala Phe Ser
355 360 365

tcg att gtt cgc acg gcg atg tcc tac atc aca atg ctg aga tca ttc 1152
Ser Ile Val Arg Thr Ala Met Ser Tyr Ile Thr Met Leu Arg Ser Phe
370 375 380

tcc taa 1158
Ser
385

<210> 24

<211> 385

<212> PRT

<213> Drosophila melanogaster

<400> 24

Met Asp Ser Phe Leu Gln Val Gln Lys Ser Thr Ile Ala Leu Leu Gly
1 5 10 15

Phe Asp Leu Phe Ser Glu Asn Arg Glu Met Trp Lys Arg Pro Tyr Arg
20 25 30

Ala Met Asn Val Phe Ser Ile Ala Ala Ile Phe Pro Phe Ile Leu Ala
35 40 45

Ala Val Leu His Asn Trp Lys Asn Val Leu Leu Leu Ala Asp Ala Met
50 55 60

Val Ala Leu Leu Ile Thr Ile Leu Gly Leu Phe Lys Phe Ser Met Ile
65 70 75 80

Leu Tyr Leu Arg Arg Asp Phe Lys Arg Leu Ile Asp Lys Phe Arg Leu
85 90 95

Leu Met Ser Asn Glu Ala Glu Gln Gly Glu Glu Tyr Ala Glu Ile Leu
100 105 110

Asn Ala Ala Asn Lys Gln Asp Gln Arg Met Cys Thr Leu Phe Arg Thr
115 120 125

Cys Phe Leu Leu Ala Trp Ala Leu Asn Ser Val Leu Pro Leu Val Arg
130 135 140

Met Gly Leu Ser Tyr Trp Leu Ala Gly His Ala Glu Pro Glu Leu Pro
 145 150 155 160

Phe Pro Cys Leu Phe Pro Trp Asn Ile His Ile Ile Arg Asn Tyr Val
 165 170 175

Leu Ser Phe Ile Trp Ser Ala Phe Ala Ser Thr Gly Val Val Leu Pro
 180 185 190

Ala Val Ser Leu Asp Thr Ile Phe Cys Ser Phe Thr Ser Asn Leu Cys
 195 200 205

Ala Phe Phe Lys Ile Ala Gln Tyr Lys Val Val Arg Phe Lys Gly Gly
 210 215 220

Ser Leu Lys Glu Ser Gln Ala Thr Leu Asn Lys Val Phe Ala Leu Tyr
 225 230 235 240

Gln Thr Ser Leu Asp Met Cys Asn Asp Leu Asn Gln Cys Tyr Gln Pro
 245 250 255

Ile Ile Cys Ala Gln Phe Phe Ile Ser Ser Leu Gln Leu Cys Met Leu
 260 265 270

Gly Tyr Leu Phe Ser Ile Thr Phe Ala Gln Thr Glu Gly Val Tyr Tyr
 275 280 285

Ala Ser Phe Ile Ala Thr Ile Ile Ile Gln Ala Tyr Ile Tyr Cys Tyr
 290 295 300

Cys Gly Glu Asn Leu Lys Thr Glu Ser Ala Ser Phe Glu Trp Ala Ile
 305 310 315 320

Tyr Asp Ser Pro Trp His Glu Ser Leu Gly Ala Gly Gly Ala Ser Thr
 325 330 335

Ser Ile Cys Arg Ser Leu Leu Ile Ser Met Met Arg Ala His Arg Gly
 340 345 350

Phe Arg Ile Thr Gly Tyr Phe Phe Glu Ala Asn Met Glu Ala Phe Ser
 355 360 365

Ser Ile Val Arg Thr Ala Met Ser Tyr Ile Thr Met Leu Arg Ser Phe
 370 375 380

Ser
 385

<210> 25
 <211> 1203
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1200)
 <223> DOR 47E.2, a coding region on BDGP Clone No.
 AC005638

<400> 25
 atg aac gac tcg ggt tat caa tca aat ctc agc ctt ctg cgg gtt ttt 48
 Met Asn Asp Ser Gly Tyr Gln Ser Asn Leu Ser Leu Leu Arg Val Phe
 1 5 10 15
 ctc gac gag ttc cga tcg gtt ctg cgg cag gaa agt ccc ggt ctc atc 96
 Leu Asp Glu Phe Arg Ser Val Leu Arg Gln Glu Ser Pro Gly Leu Ile
 20 25 30
 cca cgc ctg gct ttt tac tat gtt cgc gcc ttt ctg agc ttg ccc ctg 144
 Pro Arg Leu Ala Phe Tyr Tyr Val Arg Ala Phe Leu Ser Leu Pro Leu
 35 40 45
 tac cga tgg atc aac ttg ttc atc atg tgc aat gtg atg acc att ttc 192
 Tyr Arg Trp Ile Asn Leu Phe Ile Met Cys Asn Val Met Thr Ile Phe
 50 55 60
 tgg acc atg ttc gtg gcc ctg ccc gag tcg aag aac gtg atc gaa atg 240
 Trp Thr Met Phe Val Ala Leu Pro Glu Ser Lys Asn Val Ile Glu Met
 65 70 75 80
 ggc gac gac ttg gtt tgg att tcg ggg atg gca ctg gtg ttc acc aag 288
 Gly Asp Asp Leu Val Trp Ile Ser Gly Met Ala Leu Val Phe Thr Lys
 85 90 95
 atc ttt tac atg cat ttg cgt tgc gac gag atc gat gaa ctt att tcg 336
 Ile Phe Tyr Met His Leu Arg Cys Asp Glu Ile Asp Glu Leu Ile Ser
 100 105 110
 gat ttt gaa tac tac aac cgg gag ctg aga ccc cat aat atc gat gag 384
 Asp Phe Glu Tyr Tyr Asn Arg Glu Leu Arg Pro His Asn Ile Asp Glu
 115 120 125
 gag gtg ttg ggt tgg cag aga ctg tgc tac gtg ata gaa tcg ggt cta 432

Glu Val Leu Gly Trp Gln Arg Leu Cys Tyr Val Ile Glu Ser Gly Leu	
130	135 140
tat atc aac tgc ttt tgc ctg gtc aac ttc ttc agt gcc gct att ttc	480
Tyr Ile Asn Cys Phe Cys Leu Val Asn Phe Phe Ser Ala Ala Ile Phe	
145	150 155 160
ctg caa cct ctg ttg ggc gag gga aag ctg ccc ttc cac agc gtc tat	528
Leu Gln Pro Leu Leu Gly Glu Gly Lys Leu Pro Phe His Ser Val Tyr	
165	170 175
ccg ttt caa tgg cat cgc ttg gat ctg cat ccc tac acg ttc tgg ttc	576
Pro Phe Gln Trp His Arg Leu Asp Leu His Pro Tyr Thr Phe Trp Phe	
180	185 190
ctc tac atc tgg cag agt ctg acc tcg cag cac aac cta atg agc att	624
Leu Tyr Ile Trp Gln Ser Leu Thr Ser Gln His Asn Leu Met Ser Ile	
195	200 205
cta atg gtg gat atg gta ggc att tcc acg ttc ctc cag acg gcg ctc	672
Leu Met Val Asp Met Val Gly Ile Ser Thr Phe Leu Gln Thr Ala Leu	
210	215 220
aat ctc aag ttg ctt tgc atc gag ata agg aaa ctg ggg gac atg gag	720
Asn Leu Lys Leu Leu Cys Ile Glu Ile Arg Lys Leu Gly Asp Met Glu	
225	230 235 240
gtc agt gat aag agg ttc cac gag gag ttt tgt cgt gtg gtt cgc ttc	768
Val Ser Asp Lys Arg Phe His Glu Glu Phe Cys Arg Val Val Arg Phe	
245	250 255
cac cag cac att atc aaa ttg gtg ggg aaa gcc aat aga gct ttc aat	816
His Gln His Ile Ile Lys Leu Val Gly Lys Ala Asn Arg Ala Phe Asn	
260	265 270
ggc gcc ttc aat gca caa tta atg gcc agt ttc tcc ctg att tcc ata	864
Gly Ala Phe Asn Ala Gln Leu Met Ala Ser Phe Ser Leu Ile Ser Ile	
275	280 285
tcc act ttc gag acc atg gct gca gcg gct gtg gat ccc aaa atg gcc	912
Ser Thr Phe Glu Thr Met Ala Ala Ala Val Asp Pro Lys Met Ala	
290	295 300
gcc aag ttc gtg ctt ctc atg ctg gtg gca ttc att caa ctg tcg ctt	960
Ala Lys Phe Val Leu Leu Met Leu Val Ala Phe Ile Gln Leu Ser Leu	
305	310 315 320
tgg tgc gtc tct gga act ttg gtt tat act cag tca gtg gag gtg gct	1008

Trp Cys Val Ser Gly Thr Leu Val Tyr Thr Gln Ser Val Glu Val Ala
 325 330 335

cag gct gct ttt gat atc aac gat tgg cac acc aaa tcg cca ggc atc 1056
 Gln Ala Ala Phe Asp Ile Asn Asp Trp His Thr Lys Ser Pro Gly Ile
 340 345 350

cag agg gat ata tcc ttt gtg ata cta cga gcc cag aaa ccc ctg atg 1104
 Gln Arg Asp Ile Ser Phe Val Ile Leu Arg Ala Gln Lys Pro Leu Met
 355 360 365

tat gtg gcc gaa cca ttt ctg ccc ttc acc ctg gga acc tat atg ctt 1152
 Tyr Val Ala Glu Pro Phe Leu Pro Phe Thr Leu Gly Thr Tyr Met Leu
 370 375 380

gtt ctg aag aac tgc tat cgt ttg ctg gcc ctg atg caa gaa tcg atg 1200
 Val Leu Lys Asn Cys Tyr Arg Leu Leu Ala Leu Met Gln Glu Ser Met
 385 390 395 400

tag 1203

<210> 26

<211> 400

<212> PRT

<213> *Drosophila melanogaster*

<400> 26

Met Asn Asp Ser Gly Tyr Gln Ser Asn Leu Ser Leu Leu Arg Val Phe
 1 5 10 15

Leu Asp Glu Phe Arg Ser Val Leu Arg Gln Glu Ser Pro Gly Leu Ile
 20 25 30

Pro Arg Leu Ala Phe Tyr Tyr Val Arg Ala Phe Leu Ser Leu Pro Leu
 35 40 45

Tyr Arg Trp Ile Asn Leu Phe Ile Met Cys Asn Val Met Thr Ile Phe
 50 55 60

Trp Thr Met Phe Val Ala Leu Pro Glu Ser Lys Asn Val Ile Glu Met
 65 70 75 80

Gly Asp Asp Leu Val Trp Ile Ser Gly Met Ala Leu Val Phe Thr Lys
 85 90 95

Ile Phe Tyr Met His Leu Arg Cys Asp Glu Ile Asp Glu Leu Ile Ser
 100 105 110

Asp	Phe	Glu	Tyr	Tyr	Asn	Arg	Glu	Leu	Arg	Pro	His	Asn	Ile	Asp	Glu	115	120	125	
Glu	Val	Leu	Gly	Trp	Gln	Arg	Leu	Cys	Tyr	Val	Ile	Glu	Ser	Gly	Leu	130	135	140	
Tyr	Ile	Asn	Cys	Phe	Cys	Leu	Val	Asn	Phe	Phe	Ser	Ala	Ala	Ile	Phe	145	150	155	160
Leu	Gln	Pro	Leu	Leu	Gly	Glu	Gly	Lys	Leu	Pro	Phe	His	Ser	Val	Tyr	165	170	175	
Pro	Phe	Gln	Trp	His	Arg	Leu	Asp	Leu	His	Pro	Tyr	Thr	Phe	Trp	Phe	180	185	190	
Leu	Tyr	Ile	Trp	Gln	Ser	Leu	Thr	Ser	Gln	His	Asn	Leu	Met	Ser	Ile	195	200	205	
Leu	Met	Val	Asp	Met	Val	Gly	Ile	Ser	Thr	Phe	Leu	Gln	Thr	Ala	Leu	210	215	220	
Asn	Leu	Lys	Leu	Leu	Cys	Ile	Glu	Ile	Arg	Lys	Leu	Gly	Asp	Met	Glu	225	230	235	240
Val	Ser	Asp	Lys	Arg	Phe	His	Glu	Glu	Phe	Cys	Arg	Val	Val	Arg	Phe	245	250	255	
His	Gln	His	Ile	Ile	Lys	Leu	Val	Gly	Lys	Ala	Asn	Arg	Ala	Phe	Asn	260	265	270	
Gly	Ala	Phe	Asn	Ala	Gln	Leu	Met	Ala	Ser	Phe	Ser	Leu	Ile	Ser	Ile	275	280	285	
Ser	Thr	Phe	Glu	Thr	Met	Ala	Ala	Ala	Ala	Val	Asp	Pro	Lys	Met	Ala	290	295	300	
Ala	Lys	Phe	Val	Leu	Leu	Met	Leu	Val	Ala	Phe	Ile	Gln	Leu	Ser	Leu	305	310	315	320
Trp	Cys	Val	Ser	Gly	Thr	Leu	Val	Tyr	Thr	Gln	Ser	Val	Glu	Val	Ala	325	330	335	
Gln	Ala	Ala	Phe	Asp	Ile	Asn	Asp	Trp	His	Thr	Lys	Ser	Pro	Gly	Ile	340	345	350	
Gln	Arg	Asp	Ile	Ser	Phe	Val	Ile	Leu	Arg	Ala	Gln	Lys	Pro	Leu	Met	355	360	365	

Tyr Val Ala Glu Pro Phe Leu Pro Phe Thr Leu Gly Thr Tyr Met Leu
 370 375 380

Val Leu Lys Asn Cys Tyr Arg Leu Leu Ala Leu Met Gln Glu Ser Met
 385 390 395 400

<210> 27

<211> 1140

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1137)

<223> DOR 59D.1, a coding region on BDGP Clone No.
 AC005672

<400> 27

atg gca gag gtc aga gtg gac agt ctg gag ttt ttc aag agc cat tgg 48
 Met Ala Glu Val Arg Val Asp Ser Leu Glu Phe Phe Lys Ser His Trp
 1 5 10 15

acc gcc tgg cgg tac ttg gga gtg gct cat ttt cgg gtc gag aac tgg 96
 Thr Ala Trp Arg Tyr Leu Gly Val Ala His Phe Arg Val Glu Asn Trp
 20 25 30

aag aac ctt tac gtg ttt tac agc att gtg tcg aat ctt ctc gtg acc 144
 Lys Asn Leu Tyr Val Phe Tyr Ser Ile Val Ser Asn Leu Leu Val Thr
 35 40 45

ctg tgc tac ccc gtt cac ctg gga ata tcc ctc ttt cgc aac cgc acc 192
 Leu Cys Tyr Pro Val His Leu Gly Ile Ser Leu Phe Arg Asn Arg Thr
 50 55 60

atc acc gag gac atc ctc aac ctg acc acc ttt gcg acc tgc aca gcc 240
 Ile Thr Glu Asp Ile Leu Asn Leu Thr Thr Phe Ala Thr Cys Thr Ala
 65 70 75 80

tgt tcg gtg aag tgc ctg ctc tac gcc tac aac atc aag gat gtg ctg 288
 Cys Ser Val Lys Cys Leu Leu Tyr Ala Tyr Asn Ile Lys Asp Val Leu
 85 90 95

gag atg gag cgg ctg ttg agg ctt ttg gat gaa cgc gtc gtg ggt ccg 336
 Glu Met Glu Arg Leu Leu Arg Leu Leu Asp Glu Arg Val Val Gly Pro
 100 105 110

gag caa cgc agc atc tac gga caa gtg agg gtc cag ctg cga aat gtg	384
Glu Gln Arg Ser Ile Tyr Gly Gln Val Arg Val Gln Leu Arg Asn Val	
115 120 125	
cta tac gtg ttc atc ggc atc tac atg ccg tgt gcc ctg ttc gcc gag	432
Leu Tyr Val Phe Ile Gly Ile Tyr Met Pro Cys Ala Leu Phe Ala Glu	
130 135 140	
cta tcc ttt ctg ttc aag gag gag cgc ggt ctg atg tat ccc gcc tgg	480
Leu Ser Phe Leu Phe Lys Glu Glu Arg Gly Leu Met Tyr Pro Ala Trp	
145 150 155 160	
ttt ccc ttc gac tgg ctg cac tcc acc agg aac tat tac ata gcg aac	528
Phe Pro Phe Asp Trp Leu His Ser Thr Arg Asn Tyr Tyr Ile Ala Asn	
165 170 175	
gcc tat cag ata gtg ggc atc tcg ttt cag ctg ctg caa aac tat gtt	576
Ala Tyr Gln Ile Val Gly Ile Ser Phe Gln Leu Leu Gln Asn Tyr Val	
180 185 190	
agc gac tgc ttt ccg gcg gtg gtg ctg tgc ctg atc tca tcc cac atc	624
Ser Asp Cys Phe Pro Ala Val Val Leu Cys Leu Ile Ser Ser His Ile	
195 200 205	
aaa atg ttg tac aac aga ttc gag gag gtg ggc ctg gat cca gcc aga	672
Lys Met Leu Tyr Asn Arg Phe Glu Glu Val Gly Leu Asp Pro Ala Arg	
210 215 220	
gat gcg gag aag gac ctg gag gcc tgc atc acc gat cac aag cat att	720
Asp Ala Glu Lys Asp Leu Glu Ala Cys Ile Thr Asp His Lys His Ile	
225 230 235 240	
cta gaa cta ttc cga cgc atc gag gcc ttc att tcc ctg ccc atg cta	768
Leu Glu Leu Phe Arg Arg Ile Glu Ala Phe Ile Ser Leu Pro Met Leu	
245 250 255	
att cag ttc aca gtg acc gcc ttg aat gtg tgc atc ggt tta gca gcc	816
Ile Gln Phe Thr Val Thr Ala Leu Asn Val Cys Ile Gly Leu Ala Ala	
260 265 270	
ctg gtg ttt ttc gtc agc gag ccc atg gca cgg atg tac ttc atc ttc	864
Leu Val Phe Phe Val Ser Glu Pro Met Ala Arg Met Tyr Phe Ile Phe	
275 280 285	
tac tcc ctg gcc atg ccg ctg cag atc ttt ccg tcc tgc ttt ttc ggc	912
Tyr Ser Leu Ala Met Pro Leu Gln Ile Phe Pro Ser Cys Phe Phe Gly	
290 295 300	

acc gac aac gag tac tgg ttc gga cgc ctc cac tac gcg gcc ttc agt 960
 Thr Asp Asn Glu Tyr Trp Phe Gly Arg Leu His Tyr Ala Ala Phe Ser
 305 310 315 320

tgc aat tgg cac aca cag aac agg agc ttt aag cgg aaa atg atg ctg 1008
 Cys Asn Trp His Thr Gln Asn Arg Ser Phe Lys Arg Lys Met Met Leu
 325 330 335

ttc gtt gag caa tcg ttg aag aag agc acc gct gtg gct ggc gga atg 1056
 Phe Val Glu Gln Ser Leu Lys Lys Ser Thr Ala Val Ala Gly Gly Met
 340 345 350

atg cgt atc cac ctg gac acg ttc ttt tcc acc cta aag ggg gcc tac 1104
 Met Arg Ile His Leu Asp Thr Phe Phe Ser Thr Leu Lys Gly Ala Tyr
 355 360 365

tcc ctc ttt acc atc att att cgg atg aga aag tag 1140
 Ser Leu Phe Thr Ile Ile Ile Arg Met Arg Lys
 370 375

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<212> PRT

<213> *Drosophila melanogaster*

<400> 28

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Thr Ala Trp Arg Tyr Leu Gly Val Ala His Phe Arg Val Glu Asn Trp
 20 25 30

Lys Asn Leu Tyr Val Phe Tyr Ser Ile Val Ser Asn Leu Leu Val Thr
 35 40 45

Leu Cys Tyr Pro Val His Leu Gly Ile Ser Leu Phe Arg Asn Arg Thr
 50 55 60

Ile Thr Glu Asp Ile Leu Asn Leu Thr Thr Phe Ala Thr Cys Thr Ala
 65 70 75 80

Cys Ser Val Lys Cys Leu Leu Tyr Ala Tyr Asn Ile Lys Asp Val Leu
 85 90 95

Glu Met Glu Arg Leu Leu Arg Leu Leu Asp Glu Arg Val Val Gly Pro
 100 105 110

Glu Gln Arg Ser Ile Tyr Gly Gln Val Arg Val Gln Leu Arg Asn Val
 115 120 125

Leu Tyr Val Phe Ile Gly Ile Tyr Met Pro Cys Ala Leu Phe Ala Glu
 130 135 140

Leu Ser Phe Leu Phe Lys Glu Glu Arg Gly Leu Met Tyr Pro Ala Trp
 145 150 155 160

Phe Pro Phe Asp Trp Leu His Ser Thr Arg Asn Tyr Tyr Ile Ala Asn
 165 170 175

Ala Tyr Gln Ile Val Gly Ile Ser Phe Gln Leu Leu Gln Asn Tyr Val
 180 185 190

Ser Asp Cys Phe Pro Ala Val Val Leu Cys Leu Ile Ser Ser His Ile
 195 200 205

Lys Met Leu Tyr Asn Arg Phe Glu Glu Val Gly Leu Asp Pro Ala Arg
 210 215 220

Asp Ala Glu Lys Asp Leu Glu Ala Cys Ile Thr Asp His Lys His Ile
 225 230 235 240

Leu Glu Leu Phe Arg Arg Ile Glu Ala Phe Ile Ser Leu Pro Met Leu
 245 250 255

Ile Gln Phe Thr Val Thr Ala Leu Asn Val Cys Ile Gly Leu Ala Ala
 260 265 270

Leu Val Phe Phe Val Ser Glu Pro Met Ala Arg Met Tyr Phe Ile Phe
 275 280 285

Tyr Ser Leu Ala Met Pro Leu Gln Ile Phe Pro Ser Cys Phe Phe Gly
 290 295 300

Thr Asp Asn Glu Tyr Trp Phe Gly Arg Leu His Tyr Ala Ala Phe Ser
 305 310 315 320

Cys Asn Trp His Thr Gln Asn Arg Ser Phe Lys Arg Lys Met Met Leu
 325 330 335

Phe Val Glu Gln Ser Leu Lys Lys Ser Thr Ala Val Ala Gly Gly Met
 340 345 350

Met Arg Ile His Leu Asp Thr Phe Phe Ser Thr Leu Lys Gly Ala Tyr
 355 360 365

Ser Leu Phe Thr Ile Ile Ile Arg Met Arg Lys
 370 375

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 <213> Drosophila melanogaster

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 <223> DOR 2F.1, coding region of NCBI Accession No.
 AL009195

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 tac cac tgg cgc gtt tgg gag ctc act ggc ctg atg cgt cct ccg ggc 96
 Tyr His Trp Arg Val Trp Glu Leu Thr Gly Leu Met Arg Pro Pro Gly
 20 25 30
 gtt tca agc ctg ctt tac gtg gta tac tcc att acg gtc aac ttg gtg 144
 Val Ser Ser Leu Leu Tyr Val Val Tyr Ser Ile Thr Val Asn Leu Val
 35 40 45
 gtc acc gtg ctg ttt ccc ttg agc ttg ctg gcc agg ctg ctg ttc acc 192
 Val Thr Val Leu Phe Pro Leu Ser Leu Leu Ala Arg Leu Leu Phe Thr
 50 55 60
 acc aac atg gcc gga ttg tgc gag aac ctg acc ata act att acc gat 240
 Thr Asn Met Ala Gly Leu Cys Glu Asn Leu Thr Ile Thr Ile Thr Asp
 65 70 75 80
 att gtg gcc aat ttg aag ttt gcg aat gtg tac atg gtg agg aag cag 288
 Ile Val Ala Asn Leu Lys Phe Ala Asn Val Tyr Met Val Arg Lys Gln
 85 90 95
 ctc cat gag att cgc tct ctc cta agg ctc atg gac gct aga gcc cgg 336
 Leu His Glu Ile Arg Ser Leu Leu Arg Leu Met Asp Ala Arg Ala Arg
 100 105 110
 ctg gtg ggc gat ccc gag gag att tct gcc ttg agg aag gaa gtg aat 384
 Leu Val Gly Asp Pro Glu Glu Ile Ser Ala Leu Arg Lys Glu Val Asn

115	120	125	
atc gca cag ggc act ttc cgc acc ttt gcc agt att ttc gta ttt ggc			432
Ile Ala Gln Gly Thr Phe Arg Thr Phe Ala Ser Ile Phe Val Phe Gly			
130	135	140	
act act ttg agt tgc gtc cgc gtg gtc gtt cgc cca gat cga gag ctc			480
Thr Thr Leu Ser Cys Val Arg Val Val Val Arg Pro Asp Arg Glu Leu			
145	150	155	160
ctg tat ccg gcc tgg ttc ggc gtt gac tgg atg cac tcc acc aga aac			528
Leu Tyr Pro Ala Trp Phe Gly Val Asp Trp Met His Ser Thr Arg Asn			
	165	170	175
tat gtg ctc atc aat atc tac cag ctc ttc ggc ttg ata gtg cag gct			576
Tyr Val Leu Ile Asn Ile Tyr Gln Leu Phe Gly Leu Ile Val Gln Ala			
	180	185	190
ata cag aac tgc gct agt gac tcc tat ccg cct gcg ttt ctc tgc ctg			624
Ile Gln Asn Cys Ala Ser Asp Ser Tyr Pro Pro Ala Phe Leu Cys Leu			
	195	200	205
ctc acg ggt cat atg cgt gct ttg gag ctg agg gtg cgg cgg att ggc			672
Leu Thr Gly His Met Arg Ala Leu Glu Leu Arg Val Arg Arg Ile Gly			
	210	215	220
tgc agg acg gaa aag tcc aat aaa ggg cag aca tat gaa gcc tgg cgg			720
Cys Arg Thr Glu Lys Ser Asn Lys Gly Gln Thr Tyr Glu Ala Trp Arg			
225	230	235	240
gag gag gtg tac cag gaa ctc atc gag tgc atc cgc gat ctg gcg cgg			768
Glu Glu Val Tyr Gln Glu Leu Ile Glu Cys Ile Arg Asp Leu Ala Arg			
	245	250	255
gtc cat cgg ctg agg gag atc att cag cgg gtc ctt tca gtg ccc tgc			816
Val His Arg Leu Arg Glu Ile Ile Gln Arg Val Leu Ser Val Pro Cys			
	260	265	270
atg gcc cag ttc gtc tgc tcc gcc gcc gtc cag tgt acc gtc gcc atg			864
Met Ala Gln Phe Val Cys Ser Ala Ala Val Gln Cys Thr Val Ala Met			
	275	280	285
cac ttc ctg tac gta gcg gat gac cac gac cac acc gcc atg atc atc			912
His Phe Leu Tyr Val Ala Asp Asp His Asp His Thr Ala Met Ile Ile			
	290	295	300
tcg att gta ttt ttc tcg gcc gtc acc ttg gag gtg ttt gta atc tgc			960
Ser Ile Val Phe Phe Ser Ala Val Thr Leu Glu Val Phe Val Ile Cys			

305	310	315	320	
tat ttt ggg gac agg atg cgg aca cag agc gag gcg ctg tgc gat gcc				1008
Tyr Phe Gly Asp Arg Met Arg Thr Gln Ser Glu Ala Leu Cys Asp Ala				
	325	330	335	
ttc tac gat tgc aac tgg ata gaa cag ctg ccc aag ttc aag cgc gaa				1056
Phe Tyr Asp Cys Asn Trp Ile Glu Gln Leu Pro Lys Phe Lys Arg Glu				
	340	345	350	
ctg ctc ttc acc ctg gcc agg acg cag cgg cct tct ctt atc tac gca				1104
Leu Leu Phe Thr Leu Ala Arg Thr Gln Arg Pro Ser Leu Ile Tyr Ala				
	355	360	365	
ggc aac tac atc gca ctc tcg ctg gag acc ttc gag cag cag gtc atg				1152
Gly Asn Tyr Ile Ala Leu Ser Leu Glu Thr Phe Glu Gln Gln Val Met				
	370	375	380	
agg ttc aca tac tct gtt ttc aca ctc ttg ctg agg gcc aag				1194
Arg Phe Thr Tyr Ser Val Phe Thr Leu Leu Leu Arg Ala Lys				
	385	390	395	

<210> 30
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 <213> *Drosophila melanogaster*

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			20					25					30		
Val	Ser	Ser	Leu	Leu	Tyr	Val	Val	Tyr	Ser	Ile	Thr	Val	Asn	Leu	Val
		35					40					45			
Val	Thr	Val	Leu	Phe	Pro	Leu	Ser	Leu	Leu	Ala	Arg	Leu	Leu	Phe	Thr
	50					55				60					
Thr	Asn	Met	Ala	Gly	Leu	Cys	Glu	Asn	Leu	Thr	Ile	Thr	Ile	Thr	Asp
65					70				75					80	
Ile	Val	Ala	Asn	Leu	Lys	Phe	Ala	Asn	Val	Tyr	Met	Val	Arg	Lys	Gln
			85					90						95	
Leu	His	Glu	Ile	Arg	Ser	Leu	Leu	Arg	Leu	Met	Asp	Ala	Arg	Ala	Arg

100	105	110
Leu Val Gly Asp Pro Glu Glu Ile Ser Ala Leu Arg Lys Glu Val Asn		
115	120	125
Ile Ala Gln Gly Thr Phe Arg Thr Phe Ala Ser Ile Phe Val Phe Gly		
130	135	140
Thr Thr Leu Ser Cys Val Arg Val Val Val Arg Pro Asp Arg Glu Leu		
145	150	155
Leu Tyr Pro Ala Trp Phe Gly Val Asp Trp Met His Ser Thr Arg Asn		
165	170	175
Tyr Val Leu Ile Asn Ile Tyr Gln Leu Phe Gly Leu Ile Val Gln Ala		
180	185	190
Ile Gln Asn Cys Ala Ser Asp Ser Tyr Pro Pro Ala Phe Leu Cys Leu		
195	200	205
Leu Thr Gly His Met Arg Ala Leu Glu Leu Arg Val Arg Arg Ile Gly		
210	215	220
Cys Arg Thr Glu Lys Ser Asn Lys Gly Gln Thr Tyr Glu Ala Trp Arg		
225	230	235
Glu Glu Val Tyr Gln Glu Leu Ile Glu Cys Ile Arg Asp Leu Ala Arg		
245	250	255
Val His Arg Leu Arg Glu Ile Ile Gln Arg Val Leu Ser Val Pro Cys		
260	265	270
Met Ala Gln Phe Val Cys Ser Ala Ala Val Gln Cys Thr Val Ala Met		
275	280	285
His Phe Leu Tyr Val Ala Asp Asp His Asp His Thr Ala Met Ile Ile		
290	295	300
Ser Ile Val Phe Phe Ser Ala Val Thr Leu Glu Val Phe Val Ile Cys		
305	310	315
Tyr Phe Gly Asp Arg Met Arg Thr Gln Ser Glu Ala Leu Cys Asp Ala		
325	330	335
Phe Tyr Asp Cys Asn Trp Ile Glu Gln Leu Pro Lys Phe Lys Arg Glu		
340	345	350
Leu Leu Phe Thr Leu Ala Arg Thr Gln Arg Pro Ser Leu Ile Tyr Ala		

355	360	365
Gly Asn Tyr Ile Ala Leu Ser Leu Glu Thr Phe Glu Gln Gln Val Met		
370	375	380
Arg Phe Thr Tyr Ser Val Phe Thr Leu Leu Leu Arg Ala Lys		
385	390	395

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 <212> DNA
 <213> *Drosophila melanogaster*

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 AC004121

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 cggttt aag tcc cga gat gcc ttc att tac ttg gat cgg gtg atg tgg 96
 Arg Val Lys Ser Arg Asp Ala Phe Ile Tyr Leu Asp Arg Val Met Trp
 20 25 30
 tcc ttt ggc tgg aca gag cct gaa aac aaa agg tgg atc ctt cct tat 144
 Ser Phe Gly Trp Thr Glu Pro Glu Asn Lys Arg Trp Ile Leu Pro Tyr
 35 40 45
 aaa ctg tgg tta gcg ttc gtg aac ata gta atg ctc atc ctt ctg ccg 192
 Lys Leu Trp Leu Ala Phe Val Asn Ile Val Met Leu Ile Leu Leu Pro
 50 55 60
 atc tcg ata agc atc gag tac ctc cac cga ttt aaa acc ttc tcg gcg 240
 Ile Ser Ile Ser Ile Glu Tyr Leu His Arg Phe Lys Thr Phe Ser Ala
 65 70 75 80
 ggg gag ttc ctt agt tcc ctc gag att gga gtc aac atg tac gga agc 288
 Gly Glu Phe Leu Ser Ser Leu Glu Ile Gly Val Asn Met Tyr Gly Ser
 85 90 95
 tct ttt aag tgc gcc ttc acc ttg att gga ttc aag aaa aga cag gaa 336
 Ser Phe Lys Cys Ala Phe Thr Leu Ile Gly Phe Lys Lys Arg Gln Glu

100	105	110	
gct aag gtt tta ctg gat cag ctg gac aag aga tgc ctt agc gat aag			384
Ala Lys Val Leu Leu Asp Gln Leu Asp Lys Arg Cys Leu Ser Asp Lys			
115	120	125	
gag agg tcc act gtt cat cgc tat gtc gcc atg gga aac ttt ttc gat			432
Glu Arg Ser Thr Val His Arg Tyr Val Ala Met Gly Asn Phe Phe Asp			
130	135	140	
att ttg tat cac att ttt tac tcc acc ttc gtg gta atg aac ttc ccg			480
Ile Leu Tyr His Ile Phe Tyr Ser Thr Phe Val Val Met Asn Phe Pro			
145	150	155	160
tat ttt ctg ctt gag aga cgc cat gct tgg cgc atg tac ttt cca tat			528
Tyr Phe Leu Leu Glu Arg Arg His Ala Trp Arg Met Tyr Phe Pro Tyr			
165	170	175	
atc gat tcc gac gaa cag ttt tac atc tcc agc atc gcc gag tgt ttt			576
Ile Asp Ser Asp Glu Gln Phe Tyr Ile Ser Ser Ile Ala Glu Cys Phe			
180	185	190	
ctg atg acg gag gcc atc tac atg gat ctc tgt acg gac gtg tgt ccc			624
Leu Met Thr Glu Ala Ile Tyr Met Asp Leu Cys Thr Asp Val Cys Pro			
195	200	205	
ttg atc tcc atg ctt atg gct cga tgc cac att agc ctc ctg aaa cag			672
Leu Ile Ser Met Leu Met Ala Arg Cys His Ile Ser Leu Leu Lys Gln			
210	215	220	
cga ctg aga aat ctc cga tcg aag cca gga agg acc gaa gat gag tac			720
Arg Leu Arg Asn Leu Arg Ser Lys Pro Gly Arg Thr Glu Asp Glu Tyr			
225	230	235	240
ttg gag gag ctc acc gag tgc att cgg gat cat cga ttg cta ttg gac			768
Leu Glu Glu Leu Thr Glu Cys Ile Arg Asp His Arg Leu Leu Leu Asp			
245	250	255	
tat gtt gac gca ttg cga ccc gtc ttt tcg gga acc att ttt gtg cag			816
Tyr Val Asp Ala Leu Arg Pro Val Phe Ser Gly Thr Ile Phe Val Gln			
260	265	270	
ttc ctc ctg atc ggt act gta ctg ggt ctc tca atg ata aat cta atg			864
Phe Leu Leu Ile Gly Thr Val Leu Gly Leu Ser Met Ile Asn Leu Met			
275	280	285	
ttc ttc tcg aca ttt tgg act ggt gtc gcc act tgc ctt ttt atg ttc			912
Phe Phe Ser Thr Phe Trp Thr Gly Val Ala Thr Cys Leu Phe Met Phe			

290	295	300	
gac gtg tcc atg gag acg ttc ccc ttt tgc tat ttg tgc aac atg att			960
Asp Val Ser Met Glu Thr Phe Pro Phe Cys Tyr Leu Cys Asn Met Ile			
305	310	315	320
atc gat gac tgc cag gaa atg tcc aat tgc ctc ttt caa tcg gac tgg			1008
Ile Asp Asp Cys Gln Glu Met Ser Asn Cys Leu Phe Gln Ser Asp Trp			
	325	330	335
acc tct gcc gat cgt cgc tac aaa tcc acg ttg gta tac ttt ctt cac			1056
Thr Ser Ala Asp Arg Arg Tyr Lys Ser Thr Leu Val Tyr Phe Leu His			
	340	345	350
aat ctt cag caa ccc att act ctc acg gct ggt gga gtg ttt cct att			1104
Asn Leu Gln Gln Pro Ile Thr Leu Thr Ala Gly Gly Val Phe Pro Ile			
	355	360	365
tcc atg caa aca aat ttg gct atg gtg aag ctg gca ttt tct gtg gtt			1152
Ser Met Gln Thr Asn Leu Ala Met Val Lys Leu Ala Phe Ser Val Val			
	370	375	380
acg gta att aag caa ttt aac ttg gcc gaa agg ttt caa			1191
Thr Val Ile Lys Gln Phe Asn Leu Ala Glu Arg Phe Gln			
385	390	395	

<210> 32

<211> 397

<212> PRT

<213> *Drosophila melanogaster*

<400> 32

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			20					25					30		

Ser	Phe	Gly	Trp	Thr	Glu	Pro	Glu	Asn	Lys	Arg	Trp	Ile	Leu	Pro	Tyr
		35					40					45			

Lys	Leu	Trp	Leu	Ala	Phe	Val	Asn	Ile	Val	Met	Leu	Ile	Leu	Leu	Pro
	50					55					60				

Ile	Ser	Ile	Ser	Ile	Glu	Tyr	Leu	His	Arg	Phe	Lys	Thr	Phe	Ser	Ala
65					70					75					80

Gly	Glu	Phe	Leu	Ser	Ser	Leu	Glu	Ile	Gly	Val	Asn	Met	Tyr	Gly	Ser	85	90	95	
Ser	Phe	Lys	Cys	Ala	Phe	Thr	Leu	Ile	Gly	Phe	Lys	Lys	Arg	Gln	Glu	100	105	110	
Ala	Lys	Val	Leu	Leu	Asp	Gln	Leu	Asp	Lys	Arg	Cys	Leu	Ser	Asp	Lys	115	120	125	
Glu	Arg	Ser	Thr	Val	His	Arg	Tyr	Val	Ala	Met	Gly	Asn	Phe	Phe	Asp	130	135	140	
Ile	Leu	Tyr	His	Ile	Phe	Tyr	Ser	Thr	Phe	Val	Val	Met	Asn	Phe	Pro	145	150	155	160
Tyr	Phe	Leu	Leu	Glu	Arg	Arg	His	Ala	Trp	Arg	Met	Tyr	Phe	Pro	Tyr	165	170	175	
Ile	Asp	Ser	Asp	Glu	Gln	Phe	Tyr	Ile	Ser	Ser	Ile	Ala	Glu	Cys	Phe	180	185	190	
Leu	Met	Thr	Glu	Ala	Ile	Tyr	Met	Asp	Leu	Cys	Thr	Asp	Val	Cys	Pro	195	200	205	
Leu	Ile	Ser	Met	Leu	Met	Ala	Arg	Cys	His	Ile	Ser	Leu	Leu	Lys	Gln	210	215	220	
Arg	Leu	Arg	Asn	Leu	Arg	Ser	Lys	Pro	Gly	Arg	Thr	Glu	Asp	Glu	Tyr	225	230	235	240
Leu	Glu	Glu	Leu	Thr	Glu	Cys	Ile	Arg	Asp	His	Arg	Leu	Leu	Leu	Asp	245	250	255	
Tyr	Val	Asp	Ala	Leu	Arg	Pro	Val	Phe	Ser	Gly	Thr	Ile	Phe	Val	Gln	260	265	270	
Phe	Leu	Leu	Ile	Gly	Thr	Val	Leu	Gly	Leu	Ser	Met	Ile	Asn	Leu	Met	275	280	285	
Phe	Phe	Ser	Thr	Phe	Trp	Thr	Gly	Val	Ala	Thr	Cys	Leu	Phe	Met	Phe	290	295	300	
Asp	Val	Ser	Met	Glu	Thr	Phe	Pro	Phe	Cys	Tyr	Leu	Cys	Asn	Met	Ile	305	310	315	320
Ile	Asp	Asp	Cys	Gln	Glu	Met	Ser	Asn	Cys	Leu	Phe	Gln	Ser	Asp	Trp	325	330	335	

Thr Ser Ala Asp Arg Arg Tyr Lys Ser Thr Leu Val Tyr Phe Leu His
340 345 350

Asn Leu Gln Gln Pro Ile Thr Leu Thr Ala Gly Gly Val Phe Pro Ile
355 360 365

Ser Met Gln Thr Asn Leu Ala Met Val Lys Leu Ala Phe Ser Val Val
370 375 380

Thr Val Ile Lys Gln Phe Asn Leu Ala Glu Arg Phe Gln
385 390 395

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<213> Drosophila melanogaster

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<223> DOR 36E.1

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Met Val Arg Tyr Val Pro Arg Phe Ala Asp Gly Gln Lys Val Lys Leu
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gct tgg ccc ttg gcg gtt ttt cgg tta aat cac ata ttc tgg cca ttg 96
Ala Trp Pro Leu Ala Val Phe Arg Leu Asn His Ile Phe Trp Pro Leu
20 25 30

gat ccg agc aca ggg aaa tgg ggc cga tat ctg gac aag gtt cta gct 144
Asp Pro Ser Thr Gly Lys Trp Gly Arg Tyr Leu Asp Lys Val Leu Ala
35 40 45

gtt gcg atg tcc ttg gtt ttt atg caa cac aac gat gca gag ctg agg 192
Val Ala Met Ser Leu Val Phe Met Gln His Asn Asp Ala Glu Leu Arg
50 55 60

tac ttg cgc ttc gag gca agt aat cgg aat ttg gat gcc ttt ctc aca 240
Tyr Leu Arg Phe Glu Ala Ser Asn Arg Asn Leu Asp Ala Phe Leu Thr
65 70 75 80

gga atg cca acg tat tta atc ctc gtg gag gct caa ttt aga agt ctt 288
Gly Met Pro Thr Tyr Leu Ile Leu Val Glu Ala Gln Phe Arg Ser Leu
85 90 95

cac att cta ctg cac ttc gag aag ctt cag aag ttt tta gaa ata ttc	336
His Ile Leu Leu His Phe Glu Lys Leu Gln Lys Phe Leu Glu Ile Phe	
100 105 110	
tac gca aat att tat att gat ccc cgt aag gaa ccc gaa atg ttt cga	384
Tyr Ala Asn Ile Tyr Ile Asp Pro Arg Lys Glu Pro Glu Met Phe Arg	
115 120 125	
aaa gtg gat gga aag atg ata att aac aga tta gtt tcg gcc atg tac	432
Lys Val Asp Gly Lys Met Ile Ile Asn Arg Leu Val Ser Ala Met Tyr	
130 135 140	
ggg gca gtt atc tct ctg tat cta atc gca ccc gtt ttt tcc atc att	480
Gly Ala Val Ile Ser Leu Tyr Leu Ile Ala Pro Val Phe Ser Ile Ile	
145 150 155 160	
aac caa agc aaa gat ttt cta tac tct atg atc ttt ccg ttc gat tcg	528
Asn Gln Ser Lys Asp Phe Leu Tyr Ser Met Ile Phe Pro Phe Asp Ser	
165 170 175	
gat ccc ttg tac ata ttt gtg cca ctg ctt ttg aca aac gta tgg gtt	576
Asp Pro Leu Tyr Ile Phe Val Pro Leu Leu Leu Thr Asn Val Trp Val	
180 185 190	
ggc att gta ata gat acc atg atg ttc ggg gag acg aat ttg ttg tgt	624
Gly Ile Val Ile Asp Thr Met Met Phe Gly Glu Thr Asn Leu Leu Cys	
195 200 205	
gaa cta att gtc cac cta aat ggt agt tat atg ttg ctc aag agg gac	672
Glu Leu Ile Val His Leu Asn Gly Ser Tyr Met Leu Leu Lys Arg Asp	
210 215 220	
ttg cag ttg gcc att gaa aag ata tta gtt gca agg gac cgt ccg cat	720
Leu Gln Leu Ala Ile Glu Lys Ile Leu Val Ala Arg Asp Arg Pro His	
225 230 235 240	
atg gcc aaa cag cta aag gtt tta att aca aaa act ctc cga aag aat	768
Met Ala Lys Gln Leu Lys Val Leu Ile Thr Lys Thr Leu Arg Lys Asn	
245 250 255	
gtg gct cta aat cag ttt ggc cag cag ctg gag gct cag tat act gtg	816
Val Ala Leu Asn Gln Phe Gly Gln Gln Leu Glu Ala Gln Tyr Thr Val	
260 265 270	
cgg gtt ttt att atg ttt gca ttc gct gcg ggc ctt tta tgt gct ctt	864
Arg Val Phe Ile Met Phe Ala Phe Ala Ala Gly Leu Leu Cys Ala Leu	
275 280 285	

tct ttt aag gct tat acg acg gat tcc ctc agc aca atg tac tac ctt	912
Ser Phe Lys Ala Tyr Thr Thr Asp Ser Leu Ser Thr Met Tyr Tyr Leu	
290 295 300	
acc cat tgg gag caa atc ctg cag tac tct aca aat ccc agc gaa aat	960
Thr His Trp Glu Gln Ile Leu Gln Tyr Ser Thr Asn Pro Ser Glu Asn	
305 310 315 320	
ctg cga tta cta aag ctc att aac ttg gcc att gag atg aac agc aag	1008
Leu Arg Leu Leu Lys Leu Ile Asn Leu Ala Ile Glu Met Asn Ser Lys	
325 330 335	
ccc ttc tat gtg aca ggg cta aaa tat ttt cgc gtt agt ctg cag gct	1056
Pro Phe Tyr Val Thr Gly Leu Lys Tyr Phe Arg Val Ser Leu Gln Ala	
340 345 350	
ggc tta aaa gta agt gaa aaa cga gtg caa aac cat ttc act gtc agc	1104
Gly Leu Lys Val Ser Glu Lys Arg Val Gln Asn His Phe Thr Val Ser	
355 360 365	
tct ttc aca gat tct gca ggc atc ctt ctc gta ctt cac att cct cac	1152
Ser Phe Thr Asp Ser Ala Gly Ile Leu Leu Val Leu His Ile Pro His	
370 375 380	
ttc gat gca gcg acg aca aat gag caa tta aat aat tca cat ttt ttt	1200
Phe Asp Ala Ala Thr Thr Asn Glu Gln Leu Asn Asn Ser His Phe Phe	
385 390 395 400	

<210> 34

<211> 400

<212> PRT

<213> *Drosophila melanogaster*

<400> 34

Met Val Arg Tyr Val Pro Arg Phe Ala Asp Gly Gln Lys Val Lys Leu
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Ala Trp Pro Leu Ala Val Phe Arg Leu Asn His Ile Phe Trp Pro Leu
20 25 30

Asp Pro Ser Thr Gly Lys Trp Gly Arg Tyr Leu Asp Lys Val Leu Ala
35 40 45

Val Ala Met Ser Leu Val Phe Met Gln His Asn Asp Ala Glu Leu Arg
50 55 60

Tyr	Leu	Arg	Phe	Glu	Ala	Ser	Asn	Arg	Asn	Leu	Asp	Ala	Phe	Leu	Thr	65	70	75	80
Gly	Met	Pro	Thr	Tyr	Leu	Ile	Leu	Val	Glu	Ala	Gln	Phe	Arg	Ser	Leu	85	90	95	
His	Ile	Leu	Leu	His	Phe	Glu	Lys	Leu	Gln	Lys	Phe	Leu	Glu	Ile	Phe	100	105	110	
Tyr	Ala	Asn	Ile	Tyr	Ile	Asp	Pro	Arg	Lys	Glu	Pro	Glu	Met	Phe	Arg	115	120	125	
Lys	Val	Asp	Gly	Lys	Met	Ile	Ile	Asn	Arg	Leu	Val	Ser	Ala	Met	Tyr	130	135	140	
Gly	Ala	Val	Ile	Ser	Leu	Tyr	Leu	Ile	Ala	Pro	Val	Phe	Ser	Ile	Ile	145	150	155	160
Asn	Gln	Ser	Lys	Asp	Phe	Leu	Tyr	Ser	Met	Ile	Phe	Pro	Phe	Asp	Ser	165	170	175	
Asp	Pro	Leu	Tyr	Ile	Phe	Val	Pro	Leu	Leu	Leu	Thr	Asn	Val	Trp	Val	180	185	190	
Gly	Ile	Val	Ile	Asp	Thr	Met	Met	Phe	Gly	Glu	Thr	Asn	Leu	Leu	Cys	195	200	205	
Glu	Leu	Ile	Val	His	Leu	Asn	Gly	Ser	Tyr	Met	Leu	Leu	Lys	Arg	Asp	210	215	220	
Leu	Gln	Leu	Ala	Ile	Glu	Lys	Ile	Leu	Val	Ala	Arg	Asp	Arg	Pro	His	225	230	235	240
Met	Ala	Lys	Gln	Leu	Lys	Val	Leu	Ile	Thr	Lys	Thr	Leu	Arg	Lys	Asn	245	250	255	
Val	Ala	Leu	Asn	Gln	Phe	Gly	Gln	Gln	Leu	Glu	Ala	Gln	Tyr	Thr	Val	260	265	270	
Arg	Val	Phe	Ile	Met	Phe	Ala	Phe	Ala	Ala	Gly	Leu	Leu	Cys	Ala	Leu	275	280	285	
Ser	Phe	Lys	Ala	Tyr	Thr	Thr	Asp	Ser	Leu	Ser	Thr	Met	Tyr	Tyr	Leu	290	295	300	
Thr	His	Trp	Glu	Gln	Ile	Leu	Gln	Tyr	Ser	Thr	Asn	Pro	Ser	Glu	Asn	305	310	315	320

Leu Arg Leu Leu Lys Leu Ile Asn Leu Ala Ile Glu Met Asn Ser Lys
 325 330 335

Pro Phe Tyr Val Thr Gly Leu Lys Tyr Phe Arg Val Ser Leu Gln Ala
 340 345 350

Gly Leu Lys Val Ser Glu Lys Arg Val Gln Asn His Phe Thr Val Ser
 355 360 365

Ser Phe Thr Asp Ser Ala Gly Ile Leu Leu Val Leu His Ile Pro His
 370 375 380

Phe Asp Ala Ala Thr Thr Asn Glu Gln Leu Asn Asn Ser His Phe Phe
 385 390 395 400

<210> 35

<211> 1197

<212> DNA

<213> *Drosophila melanogaster*

<220>

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<223> DOR 41E.1

<400> 35

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 Met Val Phe Glu Leu Ile Arg Pro Ala Pro Leu Thr Glu Gln Lys Arg
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tcc cga gat ggt tgc atc tac ctt tac cgc gcc atg aag ttt att gga 96
 Ser Arg Asp Gly Cys Ile Tyr Leu Tyr Arg Ala Met Lys Phe Ile Gly
 20 25 30

tgg ctg ccc ccc aag cag ggt gtg ctc cgg tat gtg tac ctc acc tgg 144
 Trp Leu Pro Pro Lys Gln Gly Val Leu Arg Tyr Val Tyr Leu Thr Trp
 35 40 45

acg cta atg acg ttc gtg tgg tgt aca acg tac ctg ccg ctt ggc ttc 192
 Thr Leu Met Thr Phe Val Trp Cys Thr Thr Tyr Leu Pro Leu Gly Phe
 50 55 60

ctt ggt agc tac atg acg cag atc aag tcc ttc tcc cct gga gag ttt 240
 Leu Gly Ser Tyr Met Thr Gln Ile Lys Ser Phe Ser Pro Gly Glu Phe
 65 70 75 80

ctc act tca ctc cag gtg tgc att aat gcc tac ggc tca tcg gta aaa	288
Leu Thr Ser Leu Gln Val Cys Ile Asn Ala Tyr Gly Ser Ser Val Lys	
85 90 95	
ggt gca atc aca tac tcc atg ctc tgg cgc ctt atc aag gcc aag aac	336
Val Ala Ile Thr Tyr Ser Met Leu Trp Arg Leu Ile Lys Ala Lys Asn	
100 105 110	
att ttg gac cag ctg gac ctg cgc tgc acc gcc atg gag gag cgc gaa	384
Ile Leu Asp Gln Leu Asp Leu Arg Cys Thr Ala Met Glu Glu Arg Glu	
115 120 125	
aag atc cac cta gtg gtg gcc cgc agc aac cat gcc ttt ctc atc ttc	432
Lys Ile His Leu Val Val Ala Arg Ser Asn His Ala Phe Leu Ile Phe	
130 135 140	
acc ttt gtc tac tgc gga tat gcc ggc tcc acc tac ctg agc tcg gtt	480
Thr Phe Val Tyr Cys Gly Tyr Ala Gly Ser Thr Tyr Leu Ser Ser Val	
145 150 155 160	
ctc agc ggg cgt ccg ccc tgg cag ctg tac aat ccc ttt att gat tgg	528
Leu Ser Gly Arg Pro Pro Trp Gln Leu Tyr Asn Pro Phe Ile Asp Trp	
165 170 175	
cat gac ggc aca ctc aag ctc tgg gtg gcc tcc acg ttg gag tac atg	576
His Asp Gly Thr Leu Lys Leu Trp Val Ala Ser Thr Leu Glu Tyr Met	
180 185 190	
gtg atg tca ggc gcc gtt ctg cag gat caa ctc tcg gac tct tac cca	624
Val Met Ser Gly Ala Val Leu Gln Asp Gln Leu Ser Asp Ser Tyr Pro	
195 200 205	
ttg atc tat acc ctc atc ctt cgt gct cac ttg gac atg cta agg gag	672
Leu Ile Tyr Thr Leu Ile Leu Arg Ala His Leu Asp Met Leu Arg Glu	
210 215 220	
cgc atc cga cgc ctc cgt tcc gat gag aac ctg agc gag gcc gag agc	720
Arg Ile Arg Arg Leu Arg Ser Asp Glu Asn Leu Ser Glu Ala Glu Ser	
225 230 235 240	
tat gaa gag ctg gtc aaa tgt gtg atg gac cac aag ctc att cta aga	768
Tyr Glu Glu Leu Val Lys Cys Val Met Asp His Lys Leu Ile Leu Arg	
245 250 255	
tac tgc gcg att att aaa cca gta atc cag ggg acc atc ttc aca cag	816
Tyr Cys Ala Ile Ile Lys Pro Val Ile Gln Gly Thr Ile Phe Thr Gln	
260 265 270	

ttt ctg ctg atc ggc ctg gtt ctg ggc ttc acg ctg atc aac gtg ttt	864
Phe Leu Leu Ile Gly Leu Val Leu Gly Phe Thr Leu Ile Asn Val Phe	
275 280 285	
ttc ttc tca gac atc tgg acg ggc atc gca tca ttt atg ttt gtt ata	912
Phe Phe Ser Asp Ile Trp Thr Gly Ile Ala Ser Phe Met Phe Val Ile	
290 295 300	
acc att ttg ctg cag acc ttc ccc ttc tgc tac aca tgc aac ctc atc	960
Thr Ile Leu Leu Gln Thr Phe Pro Phe Cys Tyr Thr Cys Asn Leu Ile	
305 310 315 320	
atg gag gac tgc gag tcc ttg acc cat gct att ttc cag tcc aac tgg	1008
Met Glu Asp Cys Glu Ser Leu Thr His Ala Ile Phe Gln Ser Asn Trp	
325 330 335	
gtg gat gcc agt cgt cgc tac aaa aca aca cta ctg tat ttt ctc caa	1056
Val Asp Ala Ser Arg Arg Tyr Lys Thr Thr Leu Leu Tyr Phe Leu Gln	
340 345 350	
aac gtg cag cag cct atc gtt ttc att gca ggc ggt atc ttt cag ata	1104
Asn Val Gln Gln Pro Ile Val Phe Ile Ala Gly Gly Ile Phe Gln Ile	
355 360 365	
tcc atg agc agc aac ata agt gtg gca aag ttt gct ttc tcc gtg ata	1152
Ser Met Ser Ser Asn Ile Ser Val Ala Lys Phe Ala Phe Ser Val Ile	
370 375 380	
acc att acc aag caa atg aat ata gct gac aaa ttt aag acg gac	1197
Thr Ile Thr Lys Gln Met Asn Ile Ala Asp Lys Phe Lys Thr Asp	
385 390 395	

<210> 36

<211> 399

<212> PRT

<213> *Drosophila melanogaster*

<400> 36

Met Val Phe Glu Leu Ile Arg Pro Ala Pro Leu Thr Glu Gln Lys Arg
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Ser Arg Asp Gly Cys Ile Tyr Leu Tyr Arg Ala Met Lys Phe Ile Gly
20 25 30

Trp Leu Pro Pro Lys Gln Gly Val Leu Arg Tyr Val Tyr Leu Thr Trp
35 40 45

Thr Leu Met Thr Phe Val Trp Cys Thr Thr Tyr Leu Pro Leu Gly Phe
 50 55 60

Leu Gly Ser Tyr Met Thr Gln Ile Lys Ser Phe Ser Pro Gly Glu Phe
 65 70 75 80

Leu Thr Ser Leu Gln Val Cys Ile Asn Ala Tyr Gly Ser Ser Val Lys
 85 90 95

Val Ala Ile Thr Tyr Ser Met Leu Trp Arg Leu Ile Lys Ala Lys Asn
 100 105 110

Ile Leu Asp Gln Leu Asp Leu Arg Cys Thr Ala Met Glu Glu Arg Glu
 115 120 125

Lys Ile His Leu Val Val Ala Arg Ser Asn His Ala Phe Leu Ile Phe
 130 135 140

Thr Phe Val Tyr Cys Gly Tyr Ala Gly Ser Thr Tyr Leu Ser Ser Val
 145 150 155 160

Leu Ser Gly Arg Pro Pro Trp Gln Leu Tyr Asn Pro Phe Ile Asp Trp
 165 170 175

His Asp Gly Thr Leu Lys Leu Trp Val Ala Ser Thr Leu Glu Tyr Met
 180 185 190

Val Met Ser Gly Ala Val Leu Gln Asp Gln Leu Ser Asp Ser Tyr Pro
 195 200 205

Leu Ile Tyr Thr Leu Ile Leu Arg Ala His Leu Asp Met Leu Arg Glu
 210 215 220

Arg Ile Arg Arg Leu Arg Ser Asp Glu Asn Leu Ser Glu Ala Glu Ser
 225 230 235 240

Tyr Glu Glu Leu Val Lys Cys Val Met Asp His Lys Leu Ile Leu Arg
 245 250 255

Tyr Cys Ala Ile Ile Lys Pro Val Ile Gln Gly Thr Ile Phe Thr Gln
 260 265 270

Phe Leu Leu Ile Gly Leu Val Leu Gly Phe Thr Leu Ile Asn Val Phe
 275 280 285

Phe Phe Ser Asp Ile Trp Thr Gly Ile Ala Ser Phe Met Phe Val Ile
 290 295 300

Thr Ile Leu Leu Gln Thr Phe Pro Phe Cys Tyr Thr Cys Asn Leu Ile
 305 310 315 320

Met Glu Asp Cys Glu Ser Leu Thr His Ala Ile Phe Gln Ser Asn Trp
 325 330 335

Val Asp Ala Ser Arg Arg Tyr Lys Thr Thr Leu Leu Tyr Phe Leu Gln
 340 345 350

Asn Val Gln Gln Pro Ile Val Phe Ile Ala Gly Gly Ile Phe Gln Ile
 355 360 365

Ser Met Ser Ser Asn Ile Ser Val Ala Lys Phe Ala Phe Ser Val Ile
 370 375 380

Thr Ile Thr Lys Gln Met Asn Ile Ala Asp Lys Phe Lys Thr Asp
 385 390 395

<210> 37
 <211> 1218
 <212> DNA
 <213> Drosophila melanogaster

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 <223> DOR 41E.2

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 1 5 10 15
 tcg cca gtt cgc tcc cga gac gcg acc ctg tac ctc cta cgc tgc gtc 96
 Ser Pro Val Arg Ser Arg Asp Ala Thr Leu Tyr Leu Leu Arg Cys Val
 20 25 30
 ttc tta atg ggc gtc cgc aag cca cct gcc aag ttt ttc gtg gcc tac 144
 Phe Leu Met Gly Val Arg Lys Pro Pro Ala Lys Phe Phe Val Ala Tyr
 35 40 45
 gtg ctc tgg tcc ttc gca ctg aat ttc tgc tca aca ttt tat cag cca 192
 Val Leu Trp Ser Phe Ala Leu Asn Phe Cys Ser Thr Phe Tyr Gln Pro
 50 55 60
 att ggc ttt ctc aca ggc tat ata agc cat tta tca gag ttc tcc ccg 240

Ile	Gly	Phe	Leu	Thr	Gly	Tyr	Ile	Ser	His	Leu	Ser	Glu	Phe	Ser	Pro	
65					70					75					80	
gga	gag	ttt	cta	act	tcg	ctg	cag	gtg	gcc	ttt	aat	gct	tgg	tcc	tgc	288
Gly	Glu	Phe	Leu	Thr	Ser	Leu	Gln	Val	Ala	Phe	Asn	Ala	Trp	Ser	Cys	
				85					90					95		
tct	aca	aaa	gtc	ctg	ata	gtg	tgg	gca	cta	gtt	aaq	cgc	ttt	gac	gag	336
Ser	Thr	Lys	Val	Leu	Ile	Val	Trp	Ala	Leu	Val	Lys	Arg	Phe	Asp	Glu	
			100					105					110			
gct	aat	aac	ctt	ctc	gac	gag	atg	gat	agg	cgt	atc	aca	gac	ccc	gga	384
Ala	Asn	Asn	Leu	Leu	Asp	Glu	Met	Asp	Arg	Arg	Ile	Thr	Asp	Pro	Gly	
		115					120					125				
gag	cgt	ctt	cag	att	cat	cgc	gct	gtc	tcc	ctc	agt	aac	cgt	ata	ttc	432
Glu	Arg	Leu	Gln	Ile	His	Arg	Ala	Val	Ser	Leu	Ser	Asn	Arg	Ile	Phe	
	130					135					140					
ttc	ttt	ttc	atg	gca	gtc	tac	atg	gtt	tat	gcc	act	aat	acg	ttt	ctg	480
Phe	Phe	Phe	Met	Ala	Val	Tyr	Met	Val	Tyr	Ala	Thr	Asn	Thr	Phe	Leu	
145					150					155					160	
tcg	gcg	atc	ttc	att	gga	agg	cca	ccg	tac	caa	aat	tac	tac	cct	ttt	528
Ser	Ala	Ile	Phe	Ile	Gly	Arg	Pro	Pro	Tyr	Gln	Asn	Tyr	Tyr	Pro	Phe	
				165					170					175		
ctg	gac	tgg	cga	tct	agc	act	ctg	cat	cta	gct	ctg	cag	gcc	ggg	ctg	576
Leu	Asp	Trp	Arg	Ser	Ser	Thr	Leu	His	Leu	Ala	Leu	Gln	Ala	Gly	Leu	
			180					185					190			
gaa	tac	ttc	gcc	atg	gct	ggc	gcc	tgc	ttc	cag	gac	gtt	tgc	gtt	gat	624
Glu	Tyr	Phe	Ala	Met	Ala	Gly	Ala	Cys	Phe	Gln	Asp	Val	Cys	Val	Asp	
		195				200						205				
tgc	tac	cca	gtc	aat	ttc	gtt	ttg	gtc	ctg	cgt	gcc	cac	atg	tcg	atc	672
Cys	Tyr	Pro	Val	Asn	Phe	Val	Leu	Val	Leu	Arg	Ala	His	Met	Ser	Ile	
	210					215					220					
ttc	gcg	gag	cgc	ctt	cga	cgt	ttg	gga	act	tat	cct	tat	gaa	agc	cag	720
Phe	Ala	Glu	Arg	Leu	Arg	Arg	Leu	Gly	Thr	Tyr	Pro	Tyr	Glu	Ser	Gln	
225					230					235					240	
gag	cag	aaa	tat	gaa	cga	ttg	gtt	cag	tgc	ata	caa	gat	cac	aaa	gta	768
Glu	Gln	Lys	Tyr	Glu	Arg	Leu	Val	Gln	Cys	Ile	Gln	Asp	His	Lys	Val	
				245				250						255		
att	ttg	cga	ttt	gtt	gac	tgc	ctg	cgt	cct	gtt	att	tct	ggg	acc	atc	816

Ile	Leu	Arg	Phe	Val	Asp	Cys	Leu	Arg	Pro	Val	Ile	Ser	Gly	Thr	Ile		
			260					265					270				
ttc	gtg	caa	ttc	ttg	gtt	gtg	ggg	ttg	gtg	ctg	ggc	ttt	acc	cta	att	864	
Phe	Val	Gln	Phe	Leu	Val	Val	Gly	Leu	Val	Leu	Gly	Phe	Thr	Leu	Ile		
		275					280					285					
aac	att	gtc	ctg	ttc	gcc	aac	ttg	gga	tcg	gcc	atc	gca	gcg	ctc	tcg	912	
Asn	Ile	Val	Leu	Phe	Ala	Asn	Leu	Gly	Ser	Ala	Ile	Ala	Ala	Leu	Ser		
		290				295					300						
ttt	atg	gcc	gca	gtg	ctt	cta	gag	acg	act	ccc	ttc	tgc	ata	ttg	tgc	960	
Phe	Met	Ala	Ala	Val	Leu	Leu	Glu	Thr	Thr	Pro	Phe	Cys	Ile	Leu	Cys		
305					310					315					320		
aat	tat	ctc	aca	gaa	gac	tgc	tac	aag	ctg	gcc	gat	gcc	ctg	ttt	cag	1008	
Asn	Tyr	Leu	Thr	Glu	Asp	Cys	Tyr	Lys	Leu	Ala	Asp	Ala	Leu	Phe	Gln		
			325					330						335			
tca	aac	tgg	att	gat	gag	gag	aaa	cga	tac	caa	aag	aca	ctc	atg	tac	1056	
Ser	Asn	Trp	Ile	Asp	Glu	Glu	Lys	Arg	Tyr	Gln	Lys	Thr	Leu	Met	Tyr		
		340					345						350				
ttc	cta	cag	aaa	ctg	cag	cag	cct	ata	acc	ttc	atg	gct	atg	aac	gtg	1104	
Phe	Leu	Gln	Lys	Leu	Gln	Gln	Pro	Ile	Thr	Phe	Met	Ala	Met	Asn	Val		
		355				360						365					
ttt	cca	ata	tct	gtg	gga	act	aac	atc	agt	gtc	aca	aaa	ttt	tcg	ttc	1152	
Phe	Pro	Ile	Ser	Val	Gly	Thr	Asn	Ile	Ser	Val	Thr	Lys	Phe	Ser	Phe		
	370				375					380							
tcc	gtc	ttt	act	ctc	gta	aaa	caa	atg	aac	ata	tct	gag	aaa	ctt	gcc	1200	
Ser	Val	Phe	Thr	Leu	Val	Lys	Gln	Met	Asn	Ile	Ser	Glu	Lys	Leu	Ala		
385				390				395						400			
aaa	tct	gaa	atg	gaa	gag											1218	
Lys	Ser	Glu	Met	Glu	Glu												
			405														

<210> 38

<211> 406

<212> PRT

<213> Drosophila melanogaster

<400> 38

Met Asp Leu Arg Arg Trp Phe Pro Thr Leu Tyr Thr Gln Ser Lys Asp

1

5

10

15

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 20 25 30
 Phe Leu Met Gly Val Arg Lys Pro Pro Ala Lys Phe Phe Val Ala Tyr
 35 40 45
 Val Leu Trp Ser Phe Ala Leu Asn Phe Cys Ser Thr Phe Tyr Gln Pro
 50 55 60
 Ile Gly Phe Leu Thr Gly Tyr Ile Ser His Leu Ser Glu Phe Ser Pro
 65 70 75 80
 Gly Glu Phe Leu Thr Ser Leu Gln Val Ala Phe Asn Ala Trp Ser Cys
 85 90 95
 Ser Thr Lys Val Leu Ile Val Trp Ala Leu Val Lys Arg Phe Asp Glu
 100 105 110
 Ala Asn Asn Leu Leu Asp Glu Met Asp Arg Arg Ile Thr Asp Pro Gly
 115 120 125
 Glu Arg Leu Gln Ile His Arg Ala Val Ser Leu Ser Asn Arg Ile Phe
 130 135 140
 Phe Phe Phe Met Ala Val Tyr Met Val Tyr Ala Thr Asn Thr Phe Leu
 145 150 155 160
 Ser Ala Ile Phe Ile Gly Arg Pro Pro Tyr Gln Asn Tyr Tyr Pro Phe
 165 170 175
 Leu Asp Trp Arg Ser Ser Thr Leu His Leu Ala Leu Gln Ala Gly Leu
 180 185 190
 Glu Tyr Phe Ala Met Ala Gly Ala Cys Phe Gln Asp Val Cys Val Asp
 195 200 205
 Cys Tyr Pro Val Asn Phe Val Leu Val Leu Arg Ala His Met Ser Ile
 210 215 220
 Phe Ala Glu Arg Leu Arg Arg Leu Gly Thr Tyr Pro Tyr Glu Ser Gln
 225 230 235 240
 Glu Gln Lys Tyr Glu Arg Leu Val Gln Cys Ile Gln Asp His Lys Val
 245 250 255
 Ile Leu Arg Phe Val Asp Cys Leu Arg Pro Val Ile Ser Gly Thr Ile
 260 265 270

Phe Val Gln Phe Leu Val Val Gly Leu Val Leu Gly Phe Thr Leu Ile
 275 280 285

Asn Ile Val Leu Phe Ala Asn Leu Gly Ser Ala Ile Ala Ala Leu Ser
 290 295 300

Phe Met Ala Ala Val Leu Leu Glu Thr Thr Pro Phe Cys Ile Leu Cys
 305 310 315 320

Asn Tyr Leu Thr Glu Asp Cys Tyr Lys Leu Ala Asp Ala Leu Phe Gln
 325 330 335

Ser Asn Trp Ile Asp Glu Glu Lys Arg Tyr Gln Lys Thr Leu Met Tyr
 340 345 350

Phe Leu Gln Lys Leu Gln Gln Pro Ile Thr Phe Met Ala Met Asn Val
 355 360 365

Phe Pro Ile Ser Val Gly Thr Asn Ile Ser Val Thr Lys Phe Ser Phe
 370 375 380

Ser Val Phe Thr Leu Val Lys Gln Met Asn Ile Ser Glu Lys Leu Ala
 385 390 395 400

Lys Ser Glu Met Glu Glu
 405

<210> 39
 <211> 1188
 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <222> (1)..(1188)
 <223> DOR 45F.1

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ttc ttc gtc acc aga tac tcc ttt ggc ctg ctg ggc ctg aga ttt ggc 96
 Phe Phe Val Thr Arg Tyr Ser Phe Gly Leu Leu Gly Leu Arg Phe Gly
 20 25 30

aaa gag caa tcg tgg ctt cac ctc ttg tgg ctg gtg ttc aat ttc gtt	144
Lys Glu Gln Ser Trp Leu His Leu Leu Trp Leu Val Phe Asn Phe Val	
35 40 45	
aac ctg gcg cac tgc tgc cag gcg gag ttc gtc ttc ggc tgg agt cac	192
Asn Leu Ala His Cys Cys Gln Ala Glu Phe Val Phe Gly Trp Ser His	
50 55 60	
ttg cgc acc agt ccc gtg gat gcc atg gac gcc ttt tgt cct ctg gcc	240
Leu Arg Thr Ser Pro Val Asp Ala Met Asp Ala Phe Cys Pro Leu Ala	
65 70 75 80	
tgc agt ttc acc acg ctc ttc aag ctg gga tgg atg tgg tgg cgt cgc	288
Cys Ser Phe Thr Thr Leu Phe Lys Leu Gly Trp Met Trp Trp Arg Arg	
85 90 95	
cag gaa gta gct gat cta atg gac cgc atc cgc ttg ctc atc ggg gag	336
Gln Glu Val Ala Asp Leu Met Asp Arg Ile Arg Leu Leu Ile Gly Glu	
100 105 110	
cag gag aag agg gag gac tcc cgg aga aag gtg gct caa agg agc tac	384
Gln Glu Lys Arg Glu Asp Ser Arg Arg Lys Val Ala Gln Arg Ser Tyr	
115 120 125	
tat ctc atg gtc acc agg tgc ggt atg ctg gtc ttc acc ctg ggc agc	432
Tyr Leu Met Val Thr Arg Cys Gly Met Leu Val Phe Thr Leu Gly Ser	
130 135 140	
att acc act gga gcc ttc gtt ctg cgt tcc ctt tgg gaa atg tgg gtg	480
Ile Thr Thr Gly Ala Phe Val Leu Arg Ser Leu Trp Glu Met Trp Val	
145 150 155 160	
cgt cgt cat cag gag ttc aaa ttc gat atg ccc ttt cgc atg ctg ttc	528
Arg Arg His Gln Glu Phe Lys Phe Asp Met Pro Phe Arg Met Leu Phe	
165 170 175	
cac gac ttt gcg cat cgc atg ccc tgg ttt cca gtt ttc tat ctc tac	576
His Asp Phe Ala His Arg Met Pro Trp Phe Pro Val Phe Tyr Leu Tyr	
180 185 190	
tcc aca tgg agt ggc cag gtc act gtg tac gcc ttt gct ggt aca gat	624
Ser Thr Trp Ser Gly Gln Val Thr Val Tyr Ala Phe Ala Gly Thr Asp	
195 200 205	
ggt ttc ttc ttt ggc ttt acc ctc tac atg gcc ttc ttg ctg cag gcc	672
Gly Phe Phe Phe Gly Phe Thr Leu Tyr Met Ala Phe Leu Leu Gln Ala	
210 215 220	

<212> PRT

<213> *Drosophila melanogaster*

<400> 40

Met	Tyr	Pro	Arg	Phe	Leu	Ser	Arg	Asn	Tyr	Pro	Leu	Ala	Lys	His	Leu
1				5					10					15	

Phe	Phe	Val	Thr	Arg	Tyr	Ser	Phe	Gly	Leu	Leu	Gly	Leu	Arg	Phe	Gly
			20					25					30		

Lys	Glu	Gln	Ser	Trp	Leu	His	Leu	Leu	Trp	Leu	Val	Phe	Asn	Phe	Val
		35					40						45		

Asn	Leu	Ala	His	Cys	Cys	Gln	Ala	Glu	Phe	Val	Phe	Gly	Trp	Ser	His
	50					55						60			

Leu	Arg	Thr	Ser	Pro	Val	Asp	Ala	Met	Asp	Ala	Phe	Cys	Pro	Leu	Ala
65					70					75					80

Cys	Ser	Phe	Thr	Thr	Leu	Phe	Lys	Leu	Gly	Trp	Met	Trp	Trp	Arg	Arg
				85					90					95	

Gln	Glu	Val	Ala	Asp	Leu	Met	Asp	Arg	Ile	Arg	Leu	Leu	Ile	Gly	Glu
			100					105					110		

Gln	Glu	Lys	Arg	Glu	Asp	Ser	Arg	Arg	Lys	Val	Ala	Gln	Arg	Ser	Tyr
		115					120					125			

Tyr	Leu	Met	Val	Thr	Arg	Cys	Gly	Met	Leu	Val	Phe	Thr	Leu	Gly	Ser
	130					135					140				

Ile	Thr	Thr	Gly	Ala	Phe	Val	Leu	Arg	Ser	Leu	Trp	Glu	Met	Trp	Val
145					150					155					160

Arg	Arg	His	Gln	Glu	Phe	Lys	Phe	Asp	Met	Pro	Phe	Arg	Met	Leu	Phe
			165						170					175	

His	Asp	Phe	Ala	His	Arg	Met	Pro	Trp	Phe	Pro	Val	Phe	Tyr	Leu	Tyr
		180						185					190		

Ser	Thr	Trp	Ser	Gly	Gln	Val	Thr	Val	Tyr	Ala	Phe	Ala	Gly	Thr	Asp
		195					200					205			

Gly	Phe	Phe	Phe	Gly	Phe	Thr	Leu	Tyr	Met	Ala	Phe	Leu	Leu	Gln	Ala
	210					215					220				

Leu	Arg	Tyr	Asp	Ile	Gln	Asp	Ala	Leu	Lys	Pro	Ile	Arg	Asp	Pro	Ser
225					230					235					240

Leu Arg Glu Ser Lys Ile Cys Cys Gln Arg Leu Ala Asp Ile Val Asp
 245 250 255

Arg His Asn Glu Ile Glu Lys Ile Val Lys Glu Phe Ser Gly Ile Met
 260 265 270

Ala Ala Pro Thr Phe Val His Phe Val Ser Ala Ser Leu Val Ile Ala
 275 280 285

Thr Ser Val Ile Asp Ile Leu Leu Tyr Ser Gly Tyr Asn Ile Ile Arg
 290 295 300

Tyr Val Val Tyr Thr Phe Thr Val Ser Ser Ala Ile Phe Leu Tyr Cys
 305 310 315 320

Tyr Gly Gly Thr Glu Met Ser Thr Glu Ser Leu Ser Leu Gly Glu Ala
 325 330 335

Ala Tyr Ser Ser Ala Trp Tyr Thr Trp Asp Arg Glu Thr Arg Arg Arg
 340 345 350

Val Phe Leu Ile Ile Leu Arg Ala Gln Arg Pro Ile Thr Val Arg Val
 355 360 365

Pro Phe Phe Ala Pro Ser Leu Pro Val Phe Thr Ser Val Ile Lys Phe
 370 375 380

Thr Gly Ser Ile Val Ala Leu Ala Lys Thr Ile Leu
 385 390 395

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<211> 1158

<212> DNA

<213> *Drosophila melanogaster*

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<222> (1)..(1158)

<223> DOR 49D.1

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 1 5 10 15

ttc tgg gcc ctg ctc tat gac aaa aac ttg agg cgt tat gtg tgc att	96
Phe Trp Ala Leu Leu Tyr Asp Lys Asn Leu Arg Arg Tyr Val Cys Ile	
20 25 30	
gga ctg gcc tca ttc cac atc ttc acc caa atc gtc tac atg atg agt	144
Gly Leu Ala Ser Phe His Ile Phe Thr Gln Ile Val Tyr Met Met Ser	
35 40 45	
acc aat gaa gga cta acc ggg ata att cgt aac tca tat atg ctc gtc	192
Thr Asn Glu Gly Leu Thr Gly Ile Ile Arg Asn Ser Tyr Met Leu Val	
50 55 60	
ctt tgg att aat acg gtg ctg cga gct tat ctc ttg ctg gcg gat cac	240
Leu Trp Ile Asn Thr Val Leu Arg Ala Tyr Leu Leu Leu Ala Asp His	
65 70 75 80	
gac aga tat ttg gct ttg atc caa aaa cta act gag gcc tat tac gat	288
Asp Arg Tyr Leu Ala Leu Ile Gln Lys Leu Thr Glu Ala Tyr Tyr Asp	
85 90 95	
tta ctg aat ctg aac gat tcg tat ata tcg gaa ata ttg gac cag gtg	336
Leu Leu Asn Leu Asn Asp Ser Tyr Ile Ser Glu Ile Leu Asp Gln Val	
100 105 110	
aac aag gtg gga aag ttg atg gct agg ggc aat ctg ttc ttt ggc atg	384
Asn Lys Val Gly Lys Leu Met Ala Arg Gly Asn Leu Phe Phe Gly Met	
115 120 125	
ctc aca tcc atg gga ttc ggt ctg tac cca ttg tcc tcc agc gaa aga	432
Leu Thr Ser Met Gly Phe Gly Leu Tyr Pro Leu Ser Ser Ser Glu Arg	
130 135 140	
gct ctt aat ttt aaa acc cac ttt cct ttt gca gtc ctg cca ttt ggc	480
Ala Leu Asn Phe Lys Thr His Phe Pro Phe Ala Val Leu Pro Phe Gly	
145 150 155 160	
agc aaa att cct ggt cta aat gag tac gag agt ccg tac tat gag atg	528
Ser Lys Ile Pro Gly Leu Asn Glu Tyr Glu Ser Pro Tyr Tyr Glu Met	
165 170 175	
tgg tac atc ttt cag atg ctc atc acc ccg atg ggc tgt tgc atg tac	576
Trp Tyr Ile Phe Gln Met Leu Ile Thr Pro Met Gly Cys Cys Met Tyr	
180 185 190	
att ccg tac acc agt ctg att gtg ggc ttg ata atg ttc ggc att gtg	624
Ile Pro Tyr Thr Ser Leu Ile Val Gly Leu Ile Met Phe Gly Ile Val	
195 200 205	

agg tgc aag gct ttg cag cat cgc ctc cgc cag gtg gcg ctt aag cat	672
Arg Cys Lys Ala Leu Gln His Arg Leu Arg Gln Val Ala Leu Lys His	
210 215 220	
ccg tac gga gat cgc gat ccc cgt gaa ctg agg gag gag atc ata gcc	720
Pro Tyr Gly Asp Arg Asp Pro Arg Glu Leu Arg Glu Glu Ile Ile Ala	
225 230 235 240	
tgc ata cgt tac cag cag agc att atc gag tac atg gat cac ata aac	768
Cys Ile Arg Tyr Gln Gln Ser Ile Ile Glu Tyr Met Asp His Ile Asn	
245 250 255	
gag ctg acc acc atg atg ttc cta ttc gaa ctg atg gcc ttt tcg gcg	816
Glu Leu Thr Thr Met Met Phe Leu Phe Glu Leu Met Ala Phe Ser Ala	
260 265 270	
ctg ctc tgt gcg ctg ctc ttt atg ctg att atc gtc agc ggc acc agt	864
Leu Leu Cys Ala Leu Leu Phe Met Leu Ile Ile Val Ser Gly Thr Ser	
275 280 285	
cag ctg ata att gtt tgc atg tac att aac atg att ctg gcc caa ata	912
Gln Leu Ile Ile Val Cys Met Tyr Ile Asn Met Ile Leu Ala Gln Ile	
290 295 300	
ctg gcc ctc tat tgg tat gca aat gag tta agg gaa cag aat ctg gcg	960
Leu Ala Leu Tyr Trp Tyr Ala Asn Glu Leu Arg Glu Gln Asn Leu Ala	
305 310 315 320	
gtg gcc acc gca gcc tac gaa acg gag tgg ttc acc ttc gac gtt cca	1008
Val Ala Thr Ala Ala Tyr Glu Thr Glu Trp Phe Thr Phe Asp Val Pro	
325 330 335	
ctg cgc aaa aac atc ctg ttc atg atg atg agg gca cag cgg cca gct	1056
Leu Arg Lys Asn Ile Leu Phe Met Met Met Arg Ala Gln Arg Pro Ala	
340 345 350	
gca ata cta ctg ggc aat ata cgc ccc atc act ttg gaa ctg ttc caa	1104
Ala Ile Leu Leu Gly Asn Ile Arg Pro Ile Thr Leu Glu Leu Phe Gln	
355 360 365	
aac cta ctg aac aca acc tat aca ttt ttt acg gtt ctc aag cga gtc	1152
Asn Leu Leu Asn Thr Thr Tyr Thr Phe Phe Thr Val Leu Lys Arg Val	
370 375 380	
tac gga	1158
Tyr Gly	
385	

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 <213> *Drosophila melanogaster*

<400> 42

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Gly Leu Ala Ser Phe His Ile Phe Thr Gln Ile Val Tyr Met Met Ser
 35 40 45

Thr Asn Glu Gly Leu Thr Gly Ile Ile Arg Asn Ser Tyr Met Leu Val
 50 55 60

Leu Trp Ile Asn Thr Val Leu Arg Ala Tyr Leu Leu Leu Ala Asp His
 65 70 75 80

Asp Arg Tyr Leu Ala Leu Ile Gln Lys Leu Thr Glu Ala Tyr Tyr Asp
 85 90 95

Leu Leu Asn Leu Asn Asp Ser Tyr Ile Ser Glu Ile Leu Asp Gln Val
 100 105 110

Asn Lys Val Gly Lys Leu Met Ala Arg Gly Asn Leu Phe Phe Gly Met
 115 120 125

Leu Thr Ser Met Gly Phe Gly Leu Tyr Pro Leu Ser Ser Ser Glu Arg
 130 135 140

Ala Leu Asn Phe Lys Thr His Phe Pro Phe Ala Val Leu Pro Phe Gly
 145 150 155 160

Ser Lys Ile Pro Gly Leu Asn Glu Tyr Glu Ser Pro Tyr Tyr Glu Met
 165 170 175

Trp Tyr Ile Phe Gln Met Leu Ile Thr Pro Met Gly Cys Cys Met Tyr
 180 185 190

Ile Pro Tyr Thr Ser Leu Ile Val Gly Leu Ile Met Phe Gly Ile Val
 195 200 205

Arg Cys Lys Ala Leu Gln His Arg Leu Arg Gln Val Ala Leu Lys His
 210 215 220

Pro Tyr Gly Asp Arg Asp Pro Arg Glu Leu Arg Glu Glu Ile Ile Ala
 225 230 235 240

Cys Ile Arg Tyr Gln Gln Ser Ile Ile Glu Tyr Met Asp His Ile Asn
 245 250 255

Glu Leu Thr Thr Met Met Phe Leu Phe Glu Leu Met Ala Phe Ser Ala
 260 265 270

Leu Leu Cys Ala Leu Leu Phe Met Leu Ile Ile Val Ser Gly Thr Ser
 275 280 285

Gln Leu Ile Ile Val Cys Met Tyr Ile Asn Met Ile Leu Ala Gln Ile
 290 295 300

Leu Ala Leu Tyr Trp Tyr Ala Asn Glu Leu Arg Glu Gln Asn Leu Ala
 305 310 315 320

Val Ala Thr Ala Ala Tyr Glu Thr Glu Trp Phe Thr Phe Asp Val Pro
 325 330 335

Leu Arg Lys Asn Ile Leu Phe Met Met Met Arg Ala Gln Arg Pro Ala
 340 345 350

Ala Ile Leu Leu Gly Asn Ile Arg Pro Ile Thr Leu Glu Leu Phe Gln
 355 360 365

Asn Leu Leu Asn Thr Thr Tyr Thr Phe Phe Thr Val Leu Lys Arg Val
 370 375 380

Tyr Gly
 385

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 <213> *Drosophila melanogaster*

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1				5					10					15			
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Leu	Ser	Pro	Thr	Thr	Phe	Glu	Asp	Pro	Ile	Phe	Gly	Thr	His	Leu	Arg		
			20					25					30				
tac	ttc	caa	tgg	tac	gga	tat	gtg	gcc	tcc	aag	gat	cag	aat	agg	cct	144	
Tyr	Phe	Gln	Trp	Tyr	Gly	Tyr	Val	Ala	Ser	Lys	Asp	Gln	Asn	Arg	Pro		
		35					40					45					
ttg	tta	agt	ctt	ata	cgg	tgc	acc	att	ttg	acg	gca	tcg	att	tgg	ctt	192	
Leu	Leu	Ser	Leu	Ile	Arg	Cys	Thr	Ile	Leu	Thr	Ala	Ser	Ile	Trp	Leu		
	50					55					60						
agc	tgt	gct	tta	atg	ctg	gcg	aga	gtg	ttt	cgt	ggg	tac	gaa	aac	ctc	240	
Ser	Cys	Ala	Leu	Met	Leu	Ala	Arg	Val	Phe	Arg	Gly	Tyr	Glu	Asn	Leu		
65					70				75					80			
aat	gat	ggg	gcc	aca	agt	tac	gcc	acc	gca	gtc	cag	tat	ttc	gcg	gta	288	
Asn	Asp	Gly	Ala	Thr	Ser	Tyr	Ala	Thr	Ala	Val	Gln	Tyr	Phe	Ala	Val		
				85					90					95			
tcg	att	gcc	atg	ttt	aat	gct	tac	gta	caa	aga	gat	aga	tat	gtt	ctt	336	
Ser	Ile	Ala	Met	Phe	Asn	Ala	Tyr	Val	Gln	Arg	Asp	Arg	Tyr	Val	Leu		
			100					105					110				
tta	tac	tta	cac	att	gtt	tta	gaa	gta	ata	tcc	ctt	ttg	cga	gtt	gcc	384	
Leu	Tyr	Leu	His	Ile	Val	Leu	Glu	Val	Ile	Ser	Leu	Leu	Arg	Val	Ala		
		115					120					125					
cac	tcg	gat	atc	cag	aac	ttg	atg	cac	gaa	gca	gat	aat	cgg	gag	atg	432	
His	Ser	Asp	Ile	Gln	Asn	Leu	Met	His	Glu	Ala	Asp	Asn	Arg	Glu	Met		
		130				135					140						
gaa	ctt	ttg	gtc	gcc	act	cag	gct	tat	aca	cga	acc	att	acc	ctg	ttg	480	
Glu	Leu	Leu	Val	Ala	Thr	Gln	Ala	Tyr	Thr	Arg	Thr	Ile	Thr	Leu	Leu		
145					150					155				160			
atc	tgg	ata	cca	tcg	gtt	att	gct	ggc	cta	atg	gcc	tat	tca	gac	tgc	528	
Ile	Trp	Ile	Pro	Ser	Val	Ile	Ala	Gly	Leu	Met	Ala	Tyr	Ser	Asp	Cys		
				165				170					175				
atc	tac	agg	agt	ctg	ttt	ctg	ccg	aaa	tcg	gtt	ttc	aat	gtg	cca	gct	576	
Ile	Tyr	Arg	Ser	Leu	Phe	Leu	Pro	Lys	Ser	Val	Phe	Asn	Val	Pro	Ala		
			180					185				190					
gtg	cga	cgt	ggg	gag	gag	cat	ccc	att	ctg	cta	ttt	cag	ctg	ttt	ccc	624	

Val	Arg	Arg	Gly	Glu	Glu	His	Pro	Ile	Leu	Leu	Phe	Gln	Leu	Phe	Pro		
	195						200					205					
ttc	gga	gaa	ctt	tgc	gat	aac	ttc	gtt	gtt	gga	tac	ttg	gga	cct	tgg	672	
Phe	Gly	Glu	Leu	Cys	Asp	Asn	Phe	Val	Val	Gly	Tyr	Leu	Gly	Pro	Trp		
	210					215					220						
tat	gct	ctg	ggc	ctg	gga	atc	acg	gct	atc	cca	ttg	tgg	cac	acc	ttt	720	
Tyr	Ala	Leu	Gly	Leu	Gly	Ile	Thr	Ala	Ile	Pro	Leu	Trp	His	Thr	Phe		
225						230				235					240		
atc	act	tgc	ctc	atg	aag	tac	gta	aat	ctc	aag	ctg	caa	ata	ctc	aac	768	
Ile	Thr	Cys	Leu	Met	Lys	Tyr	Val	Asn	Leu	Lys	Leu	Gln	Ile	Leu	Asn		
				245					250					255			
aag	cga	gtg	gag	gag	atg	gat	att	acc	cga	ctt	aat	tcc	aaa	ttg	gta	816	
Lys	Arg	Val	Glu	Glu	Met	Asp	Ile	Thr	Arg	Leu	Asn	Ser	Lys	Leu	Val		
			260					265					270				
att	ggt	cgc	cta	act	gcc	agt	gag	tta	acc	ttc	tgg	caa	atg	caa	ctc	864	
Ile	Gly	Arg	Leu	Thr	Ala	Ser	Glu	Leu	Thr	Phe	Trp	Gln	Met	Gln	Leu		
		275					280					285					
ttc	aag	gaa	ttt	gta	aag	gaa	cag	ctg	agg	att	cga	aaa	ttt	gtc	cag	912	
Phe	Lys	Glu	Phe	Val	Lys	Glu	Gln	Leu	Arg	Ile	Arg	Lys	Phe	Val	Gln		
	290					295				300							
gaa	cta	cag	tat	ctg	att	tgc	gtg	cct	gtg	atg	gca	gat	ttc	att	atc	960	
Glu	Leu	Gln	Tyr	Leu	Ile	Cys	Val	Pro	Val	Met	Ala	Asp	Phe	Ile	Ile		
305					310					315					320		
ttc	tcg	gtt	ctc	att	tgc	ttt	ctc	ttt	ttt	gcc	ttg	aca	gtt	ggc	gtt	1008	
Phe	Ser	Val	Leu	Ile	Cys	Phe	Leu	Phe	Phe	Ala	Leu	Thr	Val	Gly	Val		
			325					330					335				
cca	agc	aaa	atg	gat	tac	ttc	ttc	atg	ttc	att	tac	ctt	ttt	gtg	atg	1056	
Pro	Ser	Lys	Met	Asp	Tyr	Phe	Phe	Met	Phe	Ile	Tyr	Leu	Phe	Val	Met		
			340					345				350					
gct	ggt	ata	ttg	tgg	att	tat	cat	tgg	cat	gcc	acg	ttg	att	gtt	gaa	1104	
Ala	Gly	Ile	Leu	Trp	Ile	Tyr	His	Trp	His	Ala	Thr	Leu	Ile	Val	Glu		
		355					360				365						
tgt	cac	gat	gaa	ctg	agc	ctt	gct	tac	ttt	tct	tgc	gga	tgg	tac	aac	1152	
Cys	His	Asp	Glu	Leu	Ser	Leu	Ala	Tyr	Phe	Ser	Cys	Gly	Trp	Tyr	Asn		
	370					375					380						
ttc	gaa	atg	cct	ttg	cag	aaa	atg	ctg	gtt	ttt	atg	atg	atg	cat	gcc	1200	

Phe Glu Met Pro Leu Gln Lys Met Leu Val Phe Met Met Met His Ala
385 390 395 400

caa agg ccg atg aag atg cgc gcc ctg ctg gtc gat ttg aat ctg agg 1248
Gln Arg Pro Met Lys Met Arg Ala Leu Leu Val Asp Leu Asn Leu Arg
405 410 415

acc ttc ata gac gta agg ctg cta act gct aac tcg ata ttg gat tta 1296
Thr Phe Ile Asp Val Arg Leu Leu Thr Ala Asn Ser Ile Leu Asp Leu
420 425 430

tcg aat tca agc ctt tcc ttt cca gat tgg ccg tgg agc cta cag cta 1344
Ser Asn Ser Ser Leu Ser Phe Pro Asp Trp Pro Trp Ser Leu Gln Leu
435 440 445

ctt caa ttt gct gcg 1359
Leu Gln Phe Ala Ala
450

<210> 44
<211> 453
<212> PRT
<213> *Drosophila melanogaster*

<400> 44
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Tyr Phe Gln Trp Tyr Gly Tyr Val Ala Ser Lys Asp Gln Asn Arg Pro
35 40 45

Leu Leu Ser Leu Ile Arg Cys Thr Ile Leu Thr Ala Ser Ile Trp Leu
50 55 60

Ser Cys Ala Leu Met Leu Ala Arg Val Phe Arg Gly Tyr Glu Asn Leu
65 70 75 80

Asn Asp Gly Ala Thr Ser Tyr Ala Thr Ala Val Gln Tyr Phe Ala Val
85 90 95

Ser Ile Ala Met Phe Asn Ala Tyr Val Gln Arg Asp Arg Tyr Val Leu
100 105 110

Leu Tyr Leu His Ile Val Leu Glu Val Ile Ser Leu Leu Arg Val Ala

115	120	125
His Ser Asp Ile Gln Asn Leu Met	His Glu Ala Asp Asn Arg Glu Met	
130	135	140
Glu Leu Leu Val Ala Thr Gln Ala Tyr Thr Arg Thr Ile Thr Leu Leu		
145	150	155
Ile Trp Ile Pro Ser Val Ile Ala Gly Leu Met Ala Tyr Ser Asp Cys		
	165	170
		175
Ile Tyr Arg Ser Leu Phe Leu Pro Lys Ser Val Phe Asn Val Pro Ala		
	180	185
		190
Val Arg Arg Gly Glu Glu His Pro Ile Leu Leu Phe Gln Leu Phe Pro		
	195	200
		205
Phe Gly Glu Leu Cys Asp Asn Phe Val Val Gly Tyr Leu Gly Pro Trp		
210	215	220
Tyr Ala Leu Gly Leu Gly Ile Thr Ala Ile Pro Leu Trp His Thr Phe		
225	230	235
		240
Ile Thr Cys Leu Met Lys Tyr Val Asn Leu Lys Leu Gln Ile Leu Asn		
	245	250
		255
Lys Arg Val Glu Glu Met Asp Ile Thr Arg Leu Asn Ser Lys Leu Val		
	260	265
		270
Ile Gly Arg Leu Thr Ala Ser Glu Leu Thr Phe Trp Gln Met Gln Leu		
	275	280
		285
Phe Lys Glu Phe Val Lys Glu Gln Leu Arg Ile Arg Lys Phe Val Gln		
290	295	300
Glu Leu Gln Tyr Leu Ile Cys Val Pro Val Met Ala Asp Phe Ile Ile		
305	310	315
		320
Phe Ser Val Leu Ile Cys Phe Leu Phe Phe Ala Leu Thr Val Gly Val		
	325	330
		335
Pro Ser Lys Met Asp Tyr Phe Phe Met Phe Ile Tyr Leu Phe Val Met		
	340	345
		350
Ala Gly Ile Leu Trp Ile Tyr His Trp His Ala Thr Leu Ile Val Glu		
	355	360
		365
Cys His Asp Glu Leu Ser Leu Ala Tyr Phe Ser Cys Gly Trp Tyr Asn		

370 375 380
 Phe Glu Met Pro Leu Gln Lys Met Leu Val Phe Met Met Met His Ala
 385 390 395 400
 Gln Arg Pro Met Lys Met Arg Ala Leu Leu Val Asp Leu Asn Leu Arg
 405 410 415
 Thr Phe Ile Asp Val Arg Leu Leu Thr Ala Asn Ser Ile Leu Asp Leu
 420 425 430
 Ser Asn Ser Ser Leu Ser Phe Pro Asp Trp Pro Trp Ser Leu Gln Leu
 435 440 445
 Leu Gln Phe Ala Ala
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<210> 45
 <211> 1278
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
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 <222> (1)..(1278)
 <223> DOR 69F.1

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 gca tgc ata cca aga tat caa tgg aaa gga cgc cct act gaa aga cag 96
 Ala Cys Ile Pro Arg Tyr Gln Trp Lys Gly Arg Pro Thr Glu Arg Gln
 20 25 30
 ttc tac gct tcg gag caa agg ata gtg ttc ctt ctt gga acc att tgc 144
 Phe Tyr Ala Ser Glu Gln Arg Ile Val Phe Leu Leu Gly Thr Ile Cys
 35 40 45
 cag ata ttc cag att act gga gtg ctt atc tat tgg tat tgc aat ggc 192
 Gln Ile Phe Gln Ile Thr Gly Val Leu Ile Tyr Trp Tyr Cys Asn Gly
 50 55 60
 cgt ctt gcc acg gaa acg ggc acc ttt gtg gca caa tta tct gaa atg 240
 Arg Leu Ala Thr Glu Thr Gly Thr Phe Val Ala Gln Leu Ser Glu Met

65	70	75	80	
tgc agt tct ttt tgt cta aca ttt gtg gga ttc tgt aac gtt tat gcg				288
Cys Ser Ser Phe Cys Leu Thr Phe Val Gly Phe Cys Asn Val Tyr Ala				
	85	90	95	
atc tct aca aac cgc aat caa att gaa aca tta ctc gag gag ctt cat				336
Ile Ser Thr Asn Arg Asn Gln Ile Glu Thr Leu Leu Glu Glu Leu His				
	100	105	110	
cag ata tat ccg aga tac agg aaa aat cac tat cgc tgc cag cat tat				384
Gln Ile Tyr Pro Arg Tyr Arg Lys Asn His Tyr Arg Cys Gln His Tyr				
	115	120	125	
ttt gac atg gcc atg aca ata atg aga att gag ttt ctt ttc tat atg				432
Phe Asp Met Ala Met Thr Ile Met Arg Ile Glu Phe Leu Phe Tyr Met				
	130	135	140	
atc ttg tac gtg tac tac aat agt gca cca tta tgg gtg ctt ctt tgg				480
Ile Leu Tyr Val Tyr Tyr Asn Ser Ala Pro Leu Trp Val Leu Leu Trp				
	145	150	155	160
gaa cac ttg cac gag gaa tat gat ctt agc ttc aag acg cag acc aac				528
Glu His Leu His Glu Glu Tyr Asp Leu Ser Phe Lys Thr Gln Thr Asn				
	165	170	175	
act tgg ttt cca tgg aaa gtc cat ggg tcg gca ctt gga ttt ggt atg				576
Thr Trp Phe Pro Trp Lys Val His Gly Ser Ala Leu Gly Phe Gly Met				
	180	185	190	
gct gta cta agc ata acc gtg gga tcc ttt gtg ggc gta ggt ttc agt				624
Ala Val Leu Ser Ile Thr Val Gly Ser Phe Val Gly Val Gly Phe Ser				
	195	200	205	
att gtc acc cag aat ctt atc tgt ttg tta acc ttc caa cta aag ttg				672
Ile Val Thr Gln Asn Leu Ile Cys Leu Leu Thr Phe Gln Leu Lys Leu				
	210	215	220	
cac tac gat gga ata tcc agt cag tta gta tct ctc gat tgc cgt cgt				720
His Tyr Asp Gly Ile Ser Ser Gln Leu Val Ser Leu Asp Cys Arg Arg				
	225	230	235	240
cct gga gct cat aag gag ttg agc atc ctc atc gcc cac cac agc cga				768
Pro Gly Ala His Lys Glu Leu Ser Ile Leu Ile Ala His His Ser Arg				
	245	250	255	
atc ctt cag ctg ggc gac caa gtc aat gac ata atg aac ttt gta ttc				816
Ile Leu Gln Leu Gly Asp Gln Val Asn Asp Ile Met Asn Phe Val Phe				

260	265	270	
ggc tct agc cta gta ggt gcc act att gcc att tgt atg tca agt gtt			864
Gly Ser Ser Leu Val Gly Ala Thr Ile Ala Ile Cys Met Ser Ser Val			
275	280	285	
tct ata atg cta ctg gac tta gca tct gcc ttc aaa tat gcc agt ggt			912
Ser Ile Met Leu Leu Asp Leu Ala Ser Ala Phe Lys Tyr Ala Ser Gly			
290	295	300	
cta gtg gca ttc gtc ctc tac aac ttt gtc atc tgc tac atg gga acc			960
Leu Val Ala Phe Val Leu Tyr Asn Phe Val Ile Cys Tyr Met Gly Thr			
305	310	315	320
gag gtc act tta gct cgt ata aag gtc ggt aat atg ggg caa ata cga			1008
Glu Val Thr Leu Ala Arg Ile Lys Val Gly Asn Met Gly Gln Ile Arg			
325	330	335	
cag cca cgt ttt aga gca gga tgg aat ttg aga act act tta agt att			1056
Gln Pro Arg Phe Arg Ala Gly Trp Asn Leu Arg Thr Thr Leu Ser Ile			
340	345	350	
ttg aca gca ttt tgc gtc tgg cga tgt ttc cac gag gaa gat ttg tat			1104
Leu Thr Ala Phe Cys Val Trp Arg Cys Phe His Glu Glu Asp Leu Tyr			
355	360	365	
cca acg ttt cga agg gca ttc ttt ttg cta ggt aac ttt tgc ctg gct			1152
Pro Thr Phe Arg Arg Ala Phe Phe Leu Leu Gly Asn Phe Cys Leu Ala			
370	375	380	
tac caa tgt att gga gta att ata gat tgt ata gat tgg ttc ata tat			1200
Tyr Gln Cys Ile Gly Val Ile Ile Asp Cys Ile Asp Trp Phe Ile Tyr			
385	390	395	400
gga cgg aag gcg gtg gat acc caa aga ttc gtt gct gag atc tca gag			1248
Gly Arg Lys Ala Val Asp Thr Gln Arg Phe Val Ala Glu Ile Ser Glu			
405	410	415	
gct aca ggt gct cgt cgc agt tgg att ttt			1278
Ala Thr Gly Ala Arg Arg Ser Trp Ile Phe			
420	425		

<210> 46

<211> 426

<212> PRT

<213> Drosophila melanogaster

<400> 46

Met Gln Leu His Asp His Met Lys Tyr Ile Asp Leu Gly Cys Lys Met
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Ala Cys Ile Pro Arg Tyr Gln Trp Lys Gly Arg Pro Thr Glu Arg Gln
20 25 30

Phe Tyr Ala Ser Glu Gln Arg Ile Val Phe Leu Leu Gly Thr Ile Cys
35 40 45

Gln Ile Phe Gln Ile Thr Gly Val Leu Ile Tyr Trp Tyr Cys Asn Gly
50 55 60

Arg Leu Ala Thr Glu Thr Gly Thr Phe Val Ala Gln Leu Ser Glu Met
65 70 75 80

Cys Ser Ser Phe Cys Leu Thr Phe Val Gly Phe Cys Asn Val Tyr Ala
85 90 95

Ile Ser Thr Asn Arg Asn Gln Ile Glu Thr Leu Leu Glu Glu Leu His
100 105 110

Gln Ile Tyr Pro Arg Tyr Arg Lys Asn His Tyr Arg Cys Gln His Tyr
115 120 125

Phe Asp Met Ala Met Thr Ile Met Arg Ile Glu Phe Leu Phe Tyr Met
130 135 140

Ile Leu Tyr Val Tyr Tyr Asn Ser Ala Pro Leu Trp Val Leu Leu Trp
145 150 155 160

Glu His Leu His Glu Glu Tyr Asp Leu Ser Phe Lys Thr Gln Thr Asn
165 170 175

Thr Trp Phe Pro Trp Lys Val His Gly Ser Ala Leu Gly Phe Gly Met
180 185 190

Ala Val Leu Ser Ile Thr Val Gly Ser Phe Val Gly Val Gly Phe Ser
195 200 205

Ile Val Thr Gln Asn Leu Ile Cys Leu Leu Thr Phe Gln Leu Lys Leu
210 215 220

His Tyr Asp Gly Ile Ser Ser Gln Leu Val Ser Leu Asp Cys Arg Arg
225 230 235 240

Pro Gly Ala His Lys Glu Leu Ser Ile Leu Ile Ala His His Ser Arg
245 250 255

Ile Leu Gln Leu Gly Asp Gln Val Asn Asp Ile Met Asn Phe Val Phe
 260 265 270

Gly Ser Ser Leu Val Gly Ala Thr Ile Ala Ile Cys Met Ser Ser Val
 275 280 285

Ser Ile Met Leu Leu Asp Leu Ala Ser Ala Phe Lys Tyr Ala Ser Gly
 290 295 300

Leu Val Ala Phe Val Leu Tyr Asn Phe Val Ile Cys Tyr Met Gly Thr
 305 310 315 320

Glu Val Thr Leu Ala Arg Ile Lys Val Gly Asn Met Gly Gln Ile Arg
 325 330 335

Gln Pro Arg Phe Arg Ala Gly Trp Asn Leu Arg Thr Thr Leu Ser Ile
 340 345 350

Leu Thr Ala Phe Cys Val Trp Arg Cys Phe His Glu Glu Asp Leu Tyr
 355 360 365

Pro Thr Phe Arg Arg Ala Phe Phe Leu Leu Gly Asn Phe Cys Leu Ala
 370 375 380

Tyr Gln Cys Ile Gly Val Ile Ile Asp Cys Ile Asp Trp Phe Ile Tyr
 385 390 395 400

Gly Arg Lys Ala Val Asp Thr Gln Arg Phe Val Ala Glu Ile Ser Glu
 405 410 415

Ala Thr Gly Ala Arg Arg Ser Trp Ile Phe
 420 425

<210> 47

<211> 1242

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1242)

<223> DOR 69F.2

<400> 47

atg cag ttg gag gac ttt atg cgg tac ccg gac ctc gtg tgt caa gcg 48

Met	Gln	Leu	Glu	Asp	Phe	Met	Arg	Tyr	Pro	Asp	Leu	Val	Cys	Gln	Ala	
1				5					10					15		
gcc caa ctt ccc aga tac acg tgg aat ggc aga cga tcc ttg gaa gtt 96																
Ala	Gln	Leu	Pro	Arg	Tyr	Thr	Trp	Asn	Gly	Arg	Arg	Ser	Leu	Glu	Val	
			20					25					30			
aaa cgc aac ttg gca aaa cgc att atc ttc tgg ctt gga gca gta aat 144																
Lys	Arg	Asn	Leu	Ala	Lys	Arg	Ile	Ile	Phe	Trp	Leu	Gly	Ala	Val	Asn	
		35					40					45				
ttg gtt tat cac aat att ggc tgc gtc atg tat ggc tat ttc ggt gat 192																
Leu	Val	Tyr	His	Asn	Ile	Gly	Cys	Val	Met	Tyr	Gly	Tyr	Phe	Gly	Asp	
		50				55					60					
gga aga aca aag gat cca att gcg tat tta gct gaa ttg gca tct gtg 240																
Gly	Arg	Thr	Lys	Asp	Pro	Ile	Ala	Tyr	Leu	Ala	Glu	Leu	Ala	Ser	Val	
	65				70				75					80		
gcc agc atg ctt ggt ttc acc att gtg ggc acc ctc aac ttg tgg aag 288																
Ala	Ser	Met	Leu	Gly	Phe	Thr	Ile	Val	Gly	Thr	Leu	Asn	Leu	Trp	Lys	
				85				90				95				
atg ctg agc ctt aag acc cat ttt gag aac cta cta aat gaa ttc gag 336																
Met	Leu	Ser	Leu	Lys	Thr	His	Phe	Glu	Asn	Leu	Leu	Asn	Glu	Phe	Glu	
			100					105				110				
gaa tta ttt caa cta atc aag cac agg gcg tat cgc ata cac cac tat 384																
Glu	Leu	Phe	Gln	Leu	Ile	Lys	His	Arg	Ala	Tyr	Arg	Ile	His	His	Tyr	
		115					120					125				
caa gaa aag tat acg cgt cat ata cga aat aca ttt att ttc cat acc 432																
Gln	Glu	Lys	Tyr	Thr	Arg	His	Ile	Arg	Asn	Thr	Phe	Ile	Phe	His	Thr	
		130				135					140					
tct gcc gtt gtc tac tac aac tca cta cca att ctt cta atg att cgg 480																
Ser	Ala	Val	Val	Tyr	Tyr	Asn	Ser	Leu	Pro	Ile	Leu	Leu	Met	Ile	Arg	
145					150				155			160				
gaa cat ttc tcg aac tca cag cag ttg ggc tat aga att cag agt aat 528																
Glu	His	Phe	Ser	Asn	Ser	Gln	Gln	Leu	Gly	Tyr	Arg	Ile	Gln	Ser	Asn	
			165					170				175				
acc tgg tat ccc tgg cag gtt cag gga tca att cct gga ttt ttt gct 576																
Thr	Trp	Tyr	Pro	Trp	Gln	Val	Gln	Gly	Ser	Ile	Pro	Gly	Phe	Phe	Ala	
			180					185				190				
gca gtc gcc tgt caa atc ttt tcg tgc caa acc aat atg tgc gtc aat 624																

Ala Val Ala Cys Gln Ile Phe Ser Cys Gln Thr Asn Met Cys Val Asn	
195 200 205	
atg ttt atc cag ttt ctg atc aac ttt ttt ggt atc cag cta gaa ata	672
Met Phe Ile Gln Phe Leu Ile Asn Phe Phe Gly Ile Gln Leu Glu Ile	
210 215 220	
cac ttc gat ggt ttg gcc agg cag ctg gag acc atc gat gcc cgc aat	720
His Phe Asp Gly Leu Ala Arg Gln Leu Glu Thr Ile Asp Ala Arg Asn	
225 230 235 240	
ccc cat gcc aag gat caa ttg aag tat ctg att gta tat cac aca aaa	768
Pro His Ala Lys Asp Gln Leu Lys Tyr Leu Ile Val Tyr His Thr Lys	
245 250 255	
ttg ctt aat cta gcc gac aga gtt aat cga tcg ttt aac ttt acg ttt	816
Leu Leu Asn Leu Ala Asp Arg Val Asn Arg Ser Phe Asn Phe Thr Phe	
260 265 270	
ctc ata agt ctg tcg gta tcc atg ata tcc aac tgt ttt ctg gca ttt	864
Leu Ile Ser Leu Ser Val Ser Met Ile Ser Asn Cys Phe Leu Ala Phe	
275 280 285	
tcc atg acc atg ttc gac ttt ggc acc tct cta aaa cat tta ctc gga	912
Ser Met Thr Met Phe Asp Phe Gly Thr Ser Leu Lys His Leu Leu Gly	
290 295 300	
ctt ttg cta ttc atc aca tat aat ttt tca atg tgc cgc agt ggt acg	960
Leu Leu Leu Phe Ile Thr Tyr Asn Phe Ser Met Cys Arg Ser Gly Thr	
305 310 315 320	
cac ttg att tta acg agt ggc aaa gta ttg cca gcg gcc ttt tat aac	1008
His Leu Ile Leu Thr Ser Gly Lys Val Leu Pro Ala Ala Phe Tyr Asn	
325 330 335	
aat tgg tat gaa ggc gat ctt gtt tat cga agg atg ctc ctc atc ctg	1056
Asn Trp Tyr Glu Gly Asp Leu Val Tyr Arg Arg Met Leu Leu Ile Leu	
340 345 350	
atg atg cgt gct acg aaa cct tat atg tgg aaa acc tac aag ctg gca	1104
Met Met Arg Ala Thr Lys Pro Tyr Met Trp Lys Thr Tyr Lys Leu Ala	
355 360 365	
cct gta tcc ata act aca tat atg gca gtg agt ttt tcc tta ctt aca	1152
Pro Val Ser Ile Thr Thr Tyr Met Ala Val Ser Phe Ser Leu Leu Thr	
370 375 380	
tgg cat tta tta ttc aat ttt aat tca tgt gtt ggc ttt cag aca ttg	1200

Trp His Leu Leu Phe Asn Phe Asn Ser Cys Val Gly Phe Gln Thr Leu
 385 390 395 400

aag ttt tca tat caa atg ttt acc tgt gtg cgg tcc ctt aaa 1242
 Lys Phe Ser Tyr Gln Met Phe Thr Cys Val Arg Ser Leu Lys
 405 410

<210> 48

<211> 414

<212> PRT

<213> Drosophila melanogaster

<400> 48

Met Gln Leu Glu Asp Phe Met Arg Tyr Pro Asp Leu Val Cys Gln Ala
 1 5 10 15

Ala Gln Leu Pro Arg Tyr Thr Trp Asn Gly Arg Arg Ser Leu Glu Val
 20 25 30

Lys Arg Asn Leu Ala Lys Arg Ile Ile Phe Trp Leu Gly Ala Val Asn
 35 40 45

Leu Val Tyr His Asn Ile Gly Cys Val Met Tyr Gly Tyr Phe Gly Asp
 50 55 60

Gly Arg Thr Lys Asp Pro Ile Ala Tyr Leu Ala Glu Leu Ala Ser Val
 65 70 75 80

Ala Ser Met Leu Gly Phe Thr Ile Val Gly Thr Leu Asn Leu Trp Lys
 85 90 95

Met Leu Ser Leu Lys Thr His Phe Glu Asn Leu Leu Asn Glu Phe Glu
 100 105 110

Glu Leu Phe Gln Leu Ile Lys His Arg Ala Tyr Arg Ile His His Tyr
 115 120 125

Gln Glu Lys Tyr Thr Arg His Ile Arg Asn Thr Phe Ile Phe His Thr
 130 135 140

Ser Ala Val Val Tyr Tyr Asn Ser Leu Pro Ile Leu Leu Met Ile Arg
 145 150 155 160

Glu His Phe Ser Asn Ser Gln Gln Leu Gly Tyr Arg Ile Gln Ser Asn
 165 170 175

Thr Trp Tyr Pro Trp Gln Val Gln Gly Ser Ile Pro Gly Phe Phe Ala

180	185	190
Ala Val Ala Cys Gln Ile Phe Ser Cys Gln Thr Asn Met Cys Val Asn		
195	200	205
Met Phe Ile Gln Phe Leu Ile Asn Phe Phe Gly Ile Gln Leu Glu Ile		
210	215	220
His Phe Asp Gly Leu Ala Arg Gln Leu Glu Thr Ile Asp Ala Arg Asn		
225	230	235 240
Pro His Ala Lys Asp Gln Leu Lys Tyr Leu Ile Val Tyr His Thr Lys		
	245	250 255
Leu Leu Asn Leu Ala Asp Arg Val Asn Arg Ser Phe Asn Phe Thr Phe		
	260	265 270
Leu Ile Ser Leu Ser Val Ser Met Ile Ser Asn Cys Phe Leu Ala Phe		
	275	280 285
Ser Met Thr Met Phe Asp Phe Gly Thr Ser Leu Lys His Leu Leu Gly		
	290	295 300
Leu Leu Leu Phe Ile Thr Tyr Asn Phe Ser Met Cys Arg Ser Gly Thr		
305	310	315 320
His Leu Ile Leu Thr Ser Gly Lys Val Leu Pro Ala Ala Phe Tyr Asn		
	325	330 335
Asn Trp Tyr Glu Gly Asp Leu Val Tyr Arg Arg Met Leu Leu Ile Leu		
	340	345 350
Met Met Arg Ala Thr Lys Pro Tyr Met Trp Lys Thr Tyr Lys Leu Ala		
	355	360 365
Pro Val Ser Ile Thr Thr Tyr Met Ala Val Ser Phe Ser Leu Leu Thr		
	370	375 380
Trp His Leu Leu Phe Asn Phe Asn Ser Cys Val Gly Phe Gln Thr Leu		
385	390	395 400
Lys Phe Ser Tyr Gln Met Phe Thr Cys Val Arg Ser Leu Lys		
	405	410

<210> 49
 <211> 1170

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1170)

<223> DOR 85A.1

<400> 49

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Met Glu Glu Leu Met Lys Tyr Ala Ser Phe Phe Thr Gln Gln Trp Ala	
1 5 10 15	
tac ggg cat ata cca atg ggt gaa gaa tcc aaa agg aac aaa ctt ata	96
Tyr Gly His Ile Pro Met Gly Glu Glu Ser Lys Arg Asn Lys Leu Ile	
20 25 30	
ttt cac ata gtt ttt tgg tcc aat gtg att aac ctg agc ttc gtt gga	144
Phe His Ile Val Phe Trp Ser Asn Val Ile Asn Leu Ser Phe Val Gly	
35 40 45	
tta ttt gag agc att tac gtt tac agt gcc ttc atg gat aat aag ttc	192
Leu Phe Glu Ser Ile Tyr Val Tyr Ser Ala Phe Met Asp Asn Lys Phe	
50 55 60	
ctg gaa gca gtc act gcg ttg tcc tac att ggc ttc gta acc gta ggc	240
Leu Glu Ala Val Thr Ala Leu Ser Tyr Ile Gly Phe Val Thr Val Gly	
65 70 75 80	
atg agc aag atg ttc ttc atc cgg tgg aag aaa acg gct ata act gaa	288
Met Ser Lys Met Phe Phe Ile Arg Trp Lys Lys Thr Ala Ile Thr Glu	
85 90 95	
ctg att aat gaa ttg aag gag atc tat ccg aat ggt ttg atc cga gag	336
Leu Ile Asn Glu Leu Lys Glu Ile Tyr Pro Asn Gly Leu Ile Arg Glu	
100 105 110	
gaa aga tac aat ctg ccg atg tat ctg ggc acc tgc tcc aga atc agc	384
Glu Arg Tyr Asn Leu Pro Met Tyr Leu Gly Thr Cys Ser Arg Ile Ser	
115 120 125	
ctt ata tat tcc ttg ctc tac tct gtt ctc atc tgg aca ttc aac ttg	432
Leu Ile Tyr Ser Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu	
130 135 140	
ttt tgt gta atg gag tat tgg gtc tat gac aag tgg ctc aac att cga	480
Phe Cys Val Met Glu Tyr Trp Val Tyr Asp Lys Trp Leu Asn Ile Arg	
145 150 155 160	

gtg gtg ggc aaa cag ttg ccg tac ctc atg tac att cct tgg aaa tgg	528
Val Val Gly Lys Gln Leu Pro Tyr Leu Met Tyr Ile Pro Trp Lys Trp	
165 170 175	
cag gat aac tgg tcg tac tat cca ctg tta ttc tcc cag aat ttt gca	576
Gln Asp Asn Trp Ser Tyr Tyr Pro Leu Leu Phe Ser Gln Asn Phe Ala	
180 185 190	
gga tac aca tct gca gct ggt caa att tca acc gat gtc ttg ctc tgc	624
Gly Tyr Thr Ser Ala Ala Gly Gln Ile Ser Thr Asp Val Leu Leu Cys	
195 200 205	
gcg gtg gcc act cag ttg gta atg cac ttc gac ttt ctc tca aat agt	672
Ala Val Ala Thr Gln Leu Val Met His Phe Asp Phe Leu Ser Asn Ser	
210 215 220	
atg gaa cgc cac gaa ttg agt gga gat tgg aag aag gac tcc cga ttt	720
Met Glu Arg His Glu Leu Ser Gly Asp Trp Lys Lys Asp Ser Arg Phe	
225 230 235 240	
ctg gtg gac att gtt agg tat cac gaa cgt ata ctc cgc ctt tca gat	768
Leu Val Asp Ile Val Arg Tyr His Glu Arg Ile Leu Arg Leu Ser Asp	
245 250 255	
gca gtg aac gat ata ttt gga att cca cta cta ctc aac ttc atg gta	816
Ala Val Asn Asp Ile Phe Gly Ile Pro Leu Leu Leu Asn Phe Met Val	
260 265 270	
tcc tcg ttc gtc atc tgc ttc gtg gga ttc cag atg act gtt gga gtt	864
Ser Ser Phe Val Ile Cys Phe Val Gly Phe Gln Met Thr Val Gly Val	
275 280 285	
ccg ccg gat ata gtt gtg aag ctc ttc ctc ttc ctt gtc tct tcg atg	912
Pro Pro Asp Ile Val Val Lys Leu Phe Leu Phe Leu Val Ser Ser Met	
290 295 300	
agt cag gtc tat ttg att tgt cac tat ggt caa ctg gtg gcc gat gct	960
Ser Gln Val Tyr Leu Ile Cys His Tyr Gly Gln Leu Val Ala Asp Ala	
305 310 315 320	
agc tac gga ttt tcg gtt gcc acc tac aat cag aag tgg tat aaa gcc	1008
Ser Tyr Gly Phe Ser Val Ala Thr Tyr Asn Gln Lys Trp Tyr Lys Ala	
325 330 335	
gat gtg cgc tat aaa cga gcc ttg gtt att att ata gct aga tcg cag	1056
Asp Val Arg Tyr Lys Arg Ala Leu Val Ile Ile Ile Ala Arg Ser Gln	
340 345 350	

aag gta act ttt cta aag gcc act ata ttc ttg gat att acc agg tcc 1104
 Lys Val Thr Phe Leu Lys Ala Thr Ile Phe Leu Asp Ile Thr Arg Ser
 355 360 365

act atg aca gat ctg ctt caa ata tca tac aaa ttc ttc gcc ctg ctg 1152
 Thr Met Thr Asp Leu Leu Gln Ile Ser Tyr Lys Phe Phe Ala Leu Leu
 370 375 380

cgc aca atg tat acc caa 1170
 Arg Thr Met Tyr Thr Gln
 385 390

<210> 50
 <211> 390
 <212> PRT
 <213> Drosophila melanogaster

<400> 50
 Met Glu Glu Leu Met Lys Tyr Ala Ser Phe Phe Thr Gln Gln Trp Ala
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Tyr Gly His Ile Pro Met Gly Glu Glu Ser Lys Arg Asn Lys Leu Ile
 20 25 30

Phe His Ile Val Phe Trp Ser Asn Val Ile Asn Leu Ser Phe Val Gly
 35 40 45

Leu Phe Glu Ser Ile Tyr Val Tyr Ser Ala Phe Met Asp Asn Lys Phe
 50 55 60

Leu Glu Ala Val Thr Ala Leu Ser Tyr Ile Gly Phe Val Thr Val Gly
 65 70 75 80

Met Ser Lys Met Phe Phe Ile Arg Trp Lys Lys Thr Ala Ile Thr Glu
 85 90 95

Leu Ile Asn Glu Leu Lys Glu Ile Tyr Pro Asn Gly Leu Ile Arg Glu
 100 105 110

Glu Arg Tyr Asn Leu Pro Met Tyr Leu Gly Thr Cys Ser Arg Ile Ser
 115 120 125

Leu Ile Tyr Ser Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu
 130 135 140

Phe Cys Val Met Glu Tyr Trp Val Tyr Asp Lys Trp Leu Asn Ile Arg

145		150		155		160
Val Val Gly Lys Gln Leu Pro Tyr Leu Met Tyr Ile Pro Trp Lys Trp						
	165		170		175	
Gln Asp Asn Trp Ser Tyr Tyr Pro Leu Leu Phe Ser Gln Asn Phe Ala						
	180		185		190	
Gly Tyr Thr Ser Ala Ala Gly Gln Ile Ser Thr Asp Val Leu Leu Cys						
	195		200		205	
Ala Val Ala Thr Gln Leu Val Met His Phe Asp Phe Leu Ser Asn Ser						
	210		215		220	
Met Glu Arg His Glu Leu Ser Gly Asp Trp Lys Lys Asp Ser Arg Phe						
	225		230		235	240
Leu Val Asp Ile Val Arg Tyr His Glu Arg Ile Leu Arg Leu Ser Asp						
	245		250		255	
Ala Val Asn Asp Ile Phe Gly Ile Pro Leu Leu Leu Asn Phe Met Val						
	260		265		270	
Ser Ser Phe Val Ile Cys Phe Val Gly Phe Gln Met Thr Val Gly Val						
	275		280		285	
Pro Pro Asp Ile Val Val Lys Leu Phe Leu Phe Leu Val Ser Ser Met						
	290		295		300	
Ser Gln Val Tyr Leu Ile Cys His Tyr Gly Gln Leu Val Ala Asp Ala						
	305		310		315	320
Ser Tyr Gly Phe Ser Val Ala Thr Tyr Asn Gln Lys Trp Tyr Lys Ala						
	325		330		335	
Asp Val Arg Tyr Lys Arg Ala Leu Val Ile Ile Ile Ala Arg Ser Gln						
	340		345		350	
Lys Val Thr Phe Leu Lys Ala Thr Ile Phe Leu Asp Ile Thr Arg Ser						
	355		360		365	
Thr Met Thr Asp Leu Leu Gln Ile Ser Tyr Lys Phe Phe Ala Leu Leu						
	370		375		380	
Arg Thr Met Tyr Thr Gln						
	385		390			

<210> 51
 <211> 1167
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1167)
 <223> DOR 85A.3

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 Met Lys Phe Met Lys Tyr Ala Val Phe Phe Tyr Thr Ser Val Gly Ile
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 gag ccg tat acg att gac tcg cgg tcc aaa aaa gcg agc cta tgg tca 96
 Glu Pro Tyr Thr Ile Asp Ser Arg Ser Lys Lys Ala Ser Leu Trp Ser
 20 25 30
 cat ctt ctc ttc tgg gcc aat gtg atc aat tta agt gtc att gtt ttc 144
 His Leu Leu Phe Trp Ala Asn Val Ile Asn Leu Ser Val Ile Val Phe
 35 40 45
 gga gag atc ctc tat ctg gga gtg gcc tat tcc gat gga aag ttc att 192
 Gly Glu Ile Leu Tyr Leu Gly Val Ala Tyr Ser Asp Gly Lys Phe Ile
 50 55 60
 gat gcc gtc act gta ctg tca tat atc gga ttc gta atc gtg ggc atg 240
 Asp Ala Val Thr Val Leu Ser Tyr Ile Gly Phe Val Ile Val Gly Met
 65 70 75 80
 agc aag atg ttc ttc ata tgg tgg aag aag acc gat cta agc gat ttg 288
 Ser Lys Met Phe Phe Ile Trp Trp Lys Lys Thr Asp Leu Ser Asp Leu
 85 90 95
 gtt aag gaa ttg gag cac atc tat cca aat ggc aaa gct gag gag gag 336
 Val Lys Glu Leu Glu His Ile Tyr Pro Asn Gly Lys Ala Glu Glu Glu
 100 105 110
 atg tat cgg ttg gat agg tat ctg cga tct tgt tca cga att agc att 384
 Met Tyr Arg Leu Asp Arg Tyr Leu Arg Ser Cys Ser Arg Ile Ser Ile
 115 120 125
 acc tat gca cta ctc tac tcc gta ctc atc tgg acc ttc aat ctg ttc 432
 Thr Tyr Ala Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu Phe
 130 135 140

agt atc atg caa ttc ctt gtc tat gaa aag ttg ctt aaa atc cga gtg	480
Ser Ile Met Gln Phe Leu Val Tyr Glu Lys Leu Leu Lys Ile Arg Val	
145 150 155 160	
gtc ggc caa acg ctg cca tat ttg atg tac ttt ccc tgg aac tgg cat	528
Val Gly Gln Thr Leu Pro Tyr Leu Met Tyr Phe Pro Trp Asn Trp His	
165 170 175	
gaa aac tgg acg tat tat gtg ctg ctg ttc tgt caa aac ttc gca gga	576
Glu Asn Trp Thr Tyr Tyr Val Leu Leu Phe Cys Gln Asn Phe Ala Gly	
180 185 190	
cat act tcg gca tcg gga cag atc tct acg gat ctt ttg ctt tgt gct	624
His Thr Ser Ala Ser Gly Gln Ile Ser Thr Asp Leu Leu Leu Cys Ala	
195 200 205	
gtt gct acc cag gtg gta atg cac ttc gat tac ttg gcc aga gtg gtg	672
Val Ala Thr Gln Val Val Met His Phe Asp Tyr Leu Ala Arg Val Val	
210 215 220	
gaa aaa caa gtg tta gat cgc gat tgg agc gaa aac tcc aga ttt ttg	720
Glu Lys Gln Val Leu Asp Arg Asp Trp Ser Glu Asn Ser Arg Phe Leu	
225 230 235 240	
gca aaa act gta caa tat cat cag cgc att ctt cgg cta atg gac gtt	768
Ala Lys Thr Val Gln Tyr His Gln Arg Ile Leu Arg Leu Met Asp Val	
245 250 255	
ctc aac gat ata ttc ggg ata ccg cta ctg ctt aac ttt atg gtc tcc	816
Leu Asn Asp Ile Phe Gly Ile Pro Leu Leu Leu Asn Phe Met Val Ser	
260 265 270	
aca ttt gtc atc tgc ttt gtg gga ttc caa atg acc gtg ggt gtc ccg	864
Thr Phe Val Ile Cys Phe Val Gly Phe Gln Met Thr Val Gly Val Pro	
275 280 285	
ccg gac atc atg att aag ctc ttc ttg ttc ctg ttc tcg tcc ttg tcg	912
Pro Asp Ile Met Ile Lys Leu Phe Leu Phe Leu Phe Ser Ser Leu Ser	
290 295 300	
caa gtg tac ttg ata tgc cac tac ggc cag ctg att gcc gat gcg agc	960
Gln Val Tyr Leu Ile Cys His Tyr Gly Gln Leu Ile Ala Asp Ala Ser	
305 310 315 320	
tct agc tta tcg att tct gca tat aag cag aat tgg caa aat gct gac	1008
Ser Ser Leu Ser Ile Ser Ala Tyr Lys Gln Asn Trp Gln Asn Ala Asp	
325 330 335	

att cgc tat cgt cgg gct ctg gta ttc ttt ata gct cga cct cag agg 1056
 Ile Arg Tyr Arg Arg Ala Leu Val Phe Phe Ile Ala Arg Pro Gln Arg
 340 345 350

aca act tat cta aaa gct aca att ttc atg aat ata aca agg gcc acc 1104
 Thr Thr Tyr Leu Lys Ala Thr Ile Phe Met Asn Ile Thr Arg Ala Thr
 355 360 365

atg acg gac ctt ctt caa gta tcc tac aaa ttt ttc gct ctg ctt cgt 1152
 Met Thr Asp Leu Leu Gln Val Ser Tyr Lys Phe Phe Ala Leu Leu Arg
 370 375 380

acc atg tac ata aag 1167
 Thr Met Tyr Ile Lys
 385

<210> 52

<211> 389

<212> PRT

<213> Drosophila melanogaster

<400> 52

Met Lys Phe Met Lys Tyr Ala Val Phe Phe Tyr Thr Ser Val Gly Ile
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Glu Pro Tyr Thr Ile Asp Ser Arg Ser Lys Lys Ala Ser Leu Trp Ser
 20 25 30

His Leu Leu Phe Trp Ala Asn Val Ile Asn Leu Ser Val Ile Val Phe
 35 40 45

Gly Glu Ile Leu Tyr Leu Gly Val Ala Tyr Ser Asp Gly Lys Phe Ile
 50 55 60

Asp Ala Val Thr Val Leu Ser Tyr Ile Gly Phe Val Ile Val Gly Met
 65 70 75 80

Ser Lys Met Phe Phe Ile Trp Trp Lys Lys Thr Asp Leu Ser Asp Leu
 85 90 95

Val Lys Glu Leu Glu His Ile Tyr Pro Asn Gly Lys Ala Glu Glu Glu
 100 105 110

Met Tyr Arg Leu Asp Arg Tyr Leu Arg Ser Cys Ser Arg Ile Ser Ile
 115 120 125

Thr Tyr Ala Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu Phe

130		135		140
Ser Ile Met Gln Phe Leu Val Tyr Glu Lys Leu Leu Lys Ile Arg Val				
145		150		155 160
Val Gly Gln Thr Leu Pro Tyr Leu Met Tyr Phe Pro Trp Asn Trp His				
	165		170	175
Glu Asn Trp Thr Tyr Tyr Val Leu Leu Phe Cys Gln Asn Phe Ala Gly				
	180		185	190
His Thr Ser Ala Ser Gly Gln Ile Ser Thr Asp Leu Leu Leu Cys Ala				
	195		200	205
Val Ala Thr Gln Val Val Met His Phe Asp Tyr Leu Ala Arg Val Val				
	210		220	
Glu Lys Gln Val Leu Asp Arg Asp Trp Ser Glu Asn Ser Arg Phe Leu				
225		230		235 240
Ala Lys Thr Val Gln Tyr His Gln Arg Ile Leu Arg Leu Met Asp Val				
	245		250	255
Leu Asn Asp Ile Phe Gly Ile Pro Leu Leu Leu Asn Phe Met Val Ser				
	260		265	270
Thr Phe Val Ile Cys Phe Val Gly Phe Gln Met Thr Val Gly Val Pro				
	275		280	285
Pro Asp Ile Met Ile Lys Leu Phe Leu Phe Leu Phe Ser Ser Leu Ser				
	290		295	300
Gln Val Tyr Leu Ile Cys His Tyr Gly Gln Leu Ile Ala Asp Ala Ser				
305		310		315 320
Ser Ser Leu Ser Ile Ser Ala Tyr Lys Gln Asn Trp Gln Asn Ala Asp				
	325		330	335
Ile Arg Tyr Arg Arg Ala Leu Val Phe Phe Ile Ala Arg Pro Gln Arg				
	340		345	350
Thr Thr Tyr Leu Lys Ala Thr Ile Phe Met Asn Ile Thr Arg Ala Thr				
	355		360	365
Met Thr Asp Leu Leu Gln Val Ser Tyr Lys Phe Phe Ala Leu Leu Arg				
	370		375	380
Thr Met Tyr Ile Lys				

<210> 53

<211> 1305

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1305)

<223> DOR 85B.1

<400> 53

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Met Gly Leu Gln Leu Ala Asn Gly Thr Lys Pro Ser Pro Arg Leu Pro	
1 5 10 15	
aaa tgg tgg cca aag cgg ctg gaa atg att ggt aaa gtg ctg ccc aaa	96
Lys Trp Trp Pro Lys Arg Leu Glu Met Ile Gly Lys Val Leu Pro Lys	
20 25 30	
gcc tat tgt tcc atg gtg att ttc acc tcc ctg cat ttg ggt gtc ctg	144
Ala Tyr Cys Ser Met Val Ile Phe Thr Ser Leu His Leu Gly Val Leu	
35 40 45	
ttc acg aaa acc aca ctg gat gtc ctg ccg acg ggg gag ctg cag gcc	192
Phe Thr Lys Thr Thr Leu Asp Val Leu Pro Thr Gly Glu Leu Gln Ala	
50 55 60	
ata acg gat gcc ctc acc atg acc ata ata tac ttt ttc acg ggc tac	240
Ile Thr Asp Ala Leu Thr Met Thr Ile Ile Tyr Phe Phe Thr Gly Tyr	
65 70 75 80	
ggc acc atc tac tgg tgc ctg cgc tcc cgg cgc ctc ttg gcc tac atg	288
Gly Thr Ile Tyr Trp Cys Leu Arg Ser Arg Arg Leu Leu Ala Tyr Met	
85 90 95	
gag cac atg aac cgg gag tat cgc cat cat tcg ctg gcc ggg gtg acc	336
Glu His Met Asn Arg Glu Tyr Arg His His Ser Leu Ala Gly Val Thr	
100 105 110	
ttt gtg agt agc cat gcg gcc ttt agg atg tcc aga aac ttc acg gtg	384
Phe Val Ser Ser His Ala Ala Phe Arg Met Ser Arg Asn Phe Thr Val	
115 120 125	
gtg tgg ata atg tcc tgc ctg ctg ggc gtg att tcc tgg ggc gtt tcg	432

Val Trp Ile Met Ser Cys Leu Leu Gly Val Ile Ser Trp Gly Val Ser	
130	135 140
cca ctg atg ctg ggc atc cgg atg ctg ccg ctc caa tgt tgg tat ccc	480
Pro Leu Met Leu Gly Ile Arg Met Leu Pro Leu Gln Cys Trp Tyr Pro	
145	150 155 160
ttc gac gcc ctg ggt ccc ggc aca tat acg gcg gtc tat gct aca caa	528
Phe Asp Ala Leu Gly Pro Gly Thr Tyr Thr Ala Val Tyr Ala Thr Gln	
	165 170 175
ctt ttc ggt cag atc atg gtg ggc atg acc ttt gga ttc ggg gga tca	576
Leu Phe Gly Gln Ile Met Val Gly Met Thr Phe Gly Phe Gly Gly Ser	
	180 185 190
ctg ttt gtc acc ctg agc ctg cta ctc ctg gga caa ttc gat gtg ctc	624
Leu Phe Val Thr Leu Ser Leu Leu Leu Leu Gly Gln Phe Asp Val Leu	
	195 200 205
tac tgc agc ctg aag aac ctg gat gcc cat acc aag ttg ctg ggc ggg	672
Tyr Cys Ser Leu Lys Asn Leu Asp Ala His Thr Lys Leu Leu Gly Gly	
	210 215 220
gag tct gta aat ggc ctg agt tcg ctg caa gag gag ttg ctg ctg ggg	720
Glu Ser Val Asn Gly Leu Ser Ser Leu Gln Glu Glu Leu Leu Leu Gly	
225	230 235 240
gac tcg aag agg gaa tta aat cag tac gtt ttg ctc cag gag cat ccg	768
Asp Ser Lys Arg Glu Leu Asn Gln Tyr Val Leu Leu Gln Glu His Pro	
	245 250 255
acg gat ctg ctg aga ttg tcg gca gga cga aaa tgt cct gac caa gga	816
Thr Asp Leu Leu Arg Leu Ser Ala Gly Arg Lys Cys Pro Asp Gln Gly	
	260 265 270
aat gcg ttt cac aac gcc ttg gtg gaa tgc att cgc ttg cat cgc ttc	864
Asn Ala Phe His Asn Ala Leu Val Glu Cys Ile Arg Leu His Arg Phe	
	275 280 285
att ctg cac tgc tca cag gag ttg gag aat cta ttc agt cca tat tgt	912
Ile Leu His Cys Ser Gln Glu Leu Glu Asn Leu Phe Ser Pro Tyr Cys	
	290 295 300
ctg gtc aag tca ctg cag atc acc ttt cag ctt tgc ctg ctg gtc ttt	960
Leu Val Lys Ser Leu Gln Ile Thr Phe Gln Leu Cys Leu Leu Val Phe	
305	310 315 320
gtg ggc gtt tcg ggt act cga gag gtc ctg cgg att gtc aac cag cta	1008

Val Gly Val Ser Gly Thr Arg Glu Val Leu Arg Ile Val Asn Gln Leu	
325 330 335	
cag tac ttg gga ctg acc atc ttc gag ctc cta atg ttc acc tat tgt	1056
Gln Tyr Leu Gly Leu Thr Ile Phe Glu Leu Leu Met Phe Thr Tyr Cys	
340 345 350	
ggc gaa ctc ctc agt cgg cat agt att cga tct ggc gac gcc ttt tgg	1104
Gly Glu Leu Leu Ser Arg His Ser Ile Arg Ser Gly Asp Ala Phe Trp	
355 360 365	
agg ggt gcg tgg tgg aag cac gcc cat ttc atc cgc cag gac atc ctc	1152
Arg Gly Ala Trp Trp Lys His Ala His Phe Ile Arg Gln Asp Ile Leu	
370 375 380	
atc ttt ctg gtc aat agt aga cgt gca gtt cac gtg act gcc ggc aag	1200
Ile Phe Leu Val Asn Ser Arg Arg Ala Val His Val Thr Ala Gly Lys	
385 390 395 400	
ttt tat gtg atg gat gtg aat cgt cta aga tcg gtt ata acg cag gcg	1248
Phe Tyr Val Met Asp Val Asn Arg Leu Arg Ser Val Ile Thr Gln Ala	
405 410 415	
ttc agc ttc ttg act ttg ctg caa aag ttg gct gcc aag aag acg gaa	1296
Phe Ser Phe Leu Thr Leu Leu Gln Lys Leu Ala Ala Lys Lys Thr Glu	
420 425 430	
tcg gag ctc	1305
Ser Glu Leu	
435	

<210> 54

<211> 435

<212> PRT

<213> Drosophila melanogaster

<400> 54

Met Gly Leu Gln Leu Ala Asn Gly Thr Lys Pro Ser Pro Arg Leu Pro
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Lys Trp Trp Pro Lys Arg Leu Glu Met Ile Gly Lys Val Leu Pro Lys
20 25 30

Ala Tyr Cys Ser Met Val Ile Phe Thr Ser Leu His Leu Gly Val Leu
35 40 45

Phe Thr Lys Thr Thr Leu Asp Val Leu Pro Thr Gly Glu Leu Gln Ala

50	55	60
Ile Thr Asp Ala Leu Thr Met Thr Ile Ile Tyr Phe Phe Thr Gly Tyr		
65	70	75 80
Gly Thr Ile Tyr Trp Cys Leu Arg Ser Arg Arg Leu Leu Ala Tyr Met		
	85	90 95
Glu His Met Asn Arg Glu Tyr Arg His His Ser Leu Ala Gly Val Thr		
	100	105 110
Phe Val Ser Ser His Ala Ala Phe Arg Met Ser Arg Asn Phe Thr Val		
	115	120 125
Val Trp Ile Met Ser Cys Leu Leu Gly Val Ile Ser Trp Gly Val Ser		
	130	135 140
Pro Leu Met Leu Gly Ile Arg Met Leu Pro Leu Gln Cys Trp Tyr Pro		
145	150	155 160
Phe Asp Ala Leu Gly Pro Gly Thr Tyr Thr Ala Val Tyr Ala Thr Gln		
	165	170 175
Leu Phe Gly Gln Ile Met Val Gly Met Thr Phe Gly Phe Gly Gly Ser		
	180	185 190
Leu Phe Val Thr Leu Ser Leu Leu Leu Leu Gly Gln Phe Asp Val Leu		
	195	200 205
Tyr Cys Ser Leu Lys Asn Leu Asp Ala His Thr Lys Leu Leu Gly Gly		
	210	215 220
Glu Ser Val Asn Gly Leu Ser Ser Leu Gln Glu Glu Leu Leu Leu Gly		
225	230	235 240
Asp Ser Lys Arg Glu Leu Asn Gln Tyr Val Leu Leu Gln Glu His Pro		
	245	250 255
Thr Asp Leu Leu Arg Leu Ser Ala Gly Arg Lys Cys Pro Asp Gln Gly		
	260	265 270
Asn Ala Phe His Asn Ala Leu Val Glu Cys Ile Arg Leu His Arg Phe		
	275	280 285
Ile Leu His Cys Ser Gln Glu Leu Glu Asn Leu Phe Ser Pro Tyr Cys		
	290	295 300
Leu Val Lys Ser Leu Gln Ile Thr Phe Gln Leu Cys Leu Leu Val Phe		

305 310 315 320
 Val Gly Val Ser Gly Thr Arg Glu Val Leu Arg Ile Val Asn Gln Leu
 325 330 335
 Gln Tyr Leu Gly Leu Thr Ile Phe Glu Leu Leu Met Phe Thr Tyr Cys
 340 345 350
 Gly Glu Leu Leu Ser Arg His Ser Ile Arg Ser Gly Asp Ala Phe Trp
 355 360 365
 Arg Gly Ala Trp Trp Lys His Ala His Phe Ile Arg Gln Asp Ile Leu
 370 375 380
 Ile Phe Leu Val Asn Ser Arg Arg Ala Val His Val Thr Ala Gly Lys
 385 390 395 400
 Phe Tyr Val Met Asp Val Asn Arg Leu Arg Ser Val Ile Thr Gln Ala
 405 410 415
 Phe Ser Phe Leu Thr Leu Leu Gln Lys Leu Ala Ala Lys Lys Thr Glu
 420 425 430
 Ser Glu Leu
 435

<210> 55
 <211> 1203
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(1203)

<400> 55
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 Met Lys Pro Thr Glu Ile Lys Lys Pro Tyr Arg Met Glu Glu Phe Leu
 1 5 10 15
 cgt ccg cag atg ttc cag gag gtg gct cag atg gtg cat ttc cag tgg 96
 Arg Pro Gln Met Phe Gln Glu Val Ala Gln Met Val His Phe Gln Trp
 20 25 30
 cgg aga aat ccg gtg gac aac agc atg gtg aac gca tcc atg gtc ccc 144
 Arg Arg Asn Pro Val Asp Asn Ser Met Val Asn Ala Ser Met Val Pro

35	40	45	
ttc tgc ttg tcg gcg ttt ctt aat gtc ctg ttt ttc ggc tgc aat ggt			192
Phe Cys Leu Ser Ala Phe Leu Asn Val Leu Phe Phe Gly Cys Asn Gly			
50	55	60	
tgg gac atc ata gga cat ttt tgg ctg gga cat cct gcc aac cag aat			240
Trp Asp Ile Ile Gly His Phe Trp Leu Gly His Pro Ala Asn Gln Asn			
65	70	75	80
ccg ccc gtg ctt agc atc acc att tac ttc tcg atc agg gga ttg atg			288
Pro Pro Val Leu Ser Ile Thr Ile Tyr Phe Ser Ile Arg Gly Leu Met			
	85	90	95
cta tac ctg aaa cga aag gaa atc gtt gag ttt gtt aac gac ttg gat			336
Leu Tyr Leu Lys Arg Lys Glu Ile Val Glu Phe Val Asn Asp Leu Asp			
	100	105	110
cgg gag tgt ccg cgg gac ttg gtc agc cag ttg gac atg caa atg gat			384
Arg Glu Cys Pro Arg Asp Leu Val Ser Gln Leu Asp Met Gln Met Asp			
	115	120	125
gag acg tac cga aac ttt tgg cag cgc tat cgc ttc atc cgt atc tac			432
Glu Thr Tyr Arg Asn Phe Trp Gln Arg Tyr Arg Phe Ile Arg Ile Tyr			
	130	135	140
tcc cat ttg ggt ggt ccg atg ttc tgc gtt gtg cca tta gct cta ttc			480
Ser His Leu Gly Gly Pro Met Phe Cys Val Val Pro Leu Ala Leu Phe			
145	150	155	160
ctc ctg acc cac gag ggt aaa gat act cct gtt gcc cag cac gag cag			528
Leu Leu Thr His Glu Gly Lys Asp Thr Pro Val Ala Gln His Glu Gln			
	165	170	175
ctc ctt gga gga tgg ctg cca tgc ggt gtg cga aag gac cca aat ttc			576
Leu Leu Gly Gly Trp Leu Pro Cys Gly Val Arg Lys Asp Pro Asn Phe			
	180	185	190
tac ctt tta gtc tgg tcc ttc gac ctg atg tgc acc act tgc ggc gtc			624
Tyr Leu Leu Val Trp Ser Phe Asp Leu Met Cys Thr Thr Cys Gly Val			
	195	200	205
tcc ttt ttc gtt acc ttc gac aac cta ttc aat gtg atg cag gga cat			672
Ser Phe Phe Val Thr Phe Asp Asn Leu Phe Asn Val Met Gln Gly His			
	210	215	220
ttg gtc atg cat ttg ggc cat ctt gct cgc cag ttt tcg gcc atc gat			720
Leu Val Met His Leu Gly His Leu Ala Arg Gln Phe Ser Ala Ile Asp			

225	230	235	240	
cct cga cag agt ttg acc gat gag aag cga ttc ttt gtg gat ctt agg				768
Pro Arg Gln Ser Leu Thr Asp Glu Lys Arg Phe Phe Val Asp Leu Arg				
	245	250	255	
tta tta gtt cag agg cag cag ctt ctt aat gga ttg tgc aga aaa tac				816
Leu Leu Val Gln Arg Gln Gln Leu Leu Asn Gly Leu Cys Arg Lys Tyr				
	260	265	270	
aac gac atc ttt aaa gtg gcc ttc ctg gtg agc aat ttt gta ggc gcc				864
Asn Asp Ile Phe Lys Val Ala Phe Leu Val Ser Asn Phe Val Gly Ala				
	275	280	285	
ggc tcc ctc tgc ttc tac ctc ttt atg ctc tcg gag aca tca gat gtc				912
Gly Ser Leu Cys Phe Tyr Leu Phe Met Leu Ser Glu Thr Ser Asp Val				
	290	295	300	
ctt atc atc gcc cag tat ata tta ccc act ttg gtc ctg gtg ggc ttc				960
Leu Ile Ile Ala Gln Tyr Ile Leu Pro Thr Leu Val Leu Val Gly Phe				
	305	310	315	320
aca ttt gag att tgt cta cgg gga acc caa ctg gaa aag gcg tcg gag				1008
Thr Phe Glu Ile Cys Leu Arg Gly Thr Gln Leu Glu Lys Ala Ser Glu				
	325	330	335	
gga ctg gaa tcg tcg ttg cga agc cag gaa tgg tat ttg gga agt agg				1056
Gly Leu Glu Ser Ser Leu Arg Ser Gln Glu Trp Tyr Leu Gly Ser Arg				
	340	345	350	
cgg tac cgg aag ttc tat ttg ctc tgg acg caa tat tgc cag cga aca				1104
Arg Tyr Arg Lys Phe Tyr Leu Leu Trp Thr Gln Tyr Cys Gln Arg Thr				
	355	360	365	
cag caa ctg ggc gcc ttt ggg cta atc caa gtc aat atg gtg cac ttc				1152
Gln Gln Leu Gly Ala Phe Gly Leu Ile Gln Val Asn Met Val His Phe				
	370	375	380	
act gaa ata atg cag ctg gcc tat aga ctc ttc act ttt ctc aaa tct				1200
Thr Glu Ile Met Gln Leu Ala Tyr Arg Leu Phe Thr Phe Leu Lys Ser				
	385	390	395	400
cat				1203
His				

<210> 56
 <211> 401

<212> PRT

<213> Drosophila melanogaster

<400> 56

Met Lys Pro Thr Glu Ile Lys Lys Pro Tyr Arg Met Glu Glu Phe Leu
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Arg Pro Gln Met Phe Gln Glu Val Ala Gln Met Val His Phe Gln Trp
20 25 30

Arg Arg Asn Pro Val Asp Asn Ser Met Val Asn Ala Ser Met Val Pro
35 40 45

Phe Cys Leu Ser Ala Phe Leu Asn Val Leu Phe Phe Gly Cys Asn Gly
50 55 60

Trp Asp Ile Ile Gly His Phe Trp Leu Gly His Pro Ala Asn Gln Asn
65 70 75 80

Pro Pro Val Leu Ser Ile Thr Ile Tyr Phe Ser Ile Arg Gly Leu Met
85 90 95

Leu Tyr Leu Lys Arg Lys Glu Ile Val Glu Phe Val Asn Asp Leu Asp
100 105 110

Arg Glu Cys Pro Arg Asp Leu Val Ser Gln Leu Asp Met Gln Met Asp
115 120 125

Glu Thr Tyr Arg Asn Phe Trp Gln Arg Tyr Arg Phe Ile Arg Ile Tyr
130 135 140

Ser His Leu Gly Gly Pro Met Phe Cys Val Val Pro Leu Ala Leu Phe
145 150 155 160

Leu Leu Thr His Glu Gly Lys Asp Thr Pro Val Ala Gln His Glu Gln
165 170 175

Leu Leu Gly Gly Trp Leu Pro Cys Gly Val Arg Lys Asp Pro Asn Phe
180 185 190

Tyr Leu Leu Val Trp Ser Phe Asp Leu Met Cys Thr Thr Cys Gly Val
195 200 205

Ser Phe Phe Val Thr Phe Asp Asn Leu Phe Asn Val Met Gln Gly His
210 215 220

Leu Val Met His Leu Gly His Leu Ala Arg Gln Phe Ser Ala Ile Asp
225 230 235 240

Pro Arg Gln Ser Leu Thr Asp Glu Lys Arg Phe Phe Val Asp Leu Arg
 245 250 255
 Leu Leu Val Gln Arg Gln Gln Leu Leu Asn Gly Leu Cys Arg Lys Tyr
 260 265 270
 Asn Asp Ile Phe Lys Val Ala Phe Leu Val Ser Asn Phe Val Gly Ala
 275 280 285
 Gly Ser Leu Cys Phe Tyr Leu Phe Met Leu Ser Glu Thr Ser Asp Val
 290 295 300
 Leu Ile Ile Ala Gln Tyr Ile Leu Pro Thr Leu Val Leu Val Gly Phe
 305 310 315 320
 Thr Phe Glu Ile Cys Leu Arg Gly Thr Gln Leu Glu Lys Ala Ser Glu
 325 330 335
 Gly Leu Glu Ser Ser Leu Arg Ser Gln Glu Trp Tyr Leu Gly Ser Arg
 340 345 350
 Arg Tyr Arg Lys Phe Tyr Leu Leu Trp Thr Gln Tyr Cys Gln Arg Thr
 355 360 365
 Gln Gln Leu Gly Ala Phe Gly Leu Ile Gln Val Asn Met Val His Phe
 370 375 380
 Thr Glu Ile Met Gln Leu Ala Tyr Arg Leu Phe Thr Phe Leu Lys Ser
 385 390 395 400
 His

<210> 57

<211> 1131

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1131)

<223> DOR 92E.1

<400> 57

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1				5					10						15		
ccg	aat	gtg	ata	agg	cgt	tac	ctg	cta	cgt	ttt	tat	ctg	gta	ctc	ggt	96	
Pro	Asn	Val	Ile	Arg	Arg	Tyr	Leu	Leu	Arg	Phe	Tyr	Leu	Val	Leu	Gly		
			20					25					30				
ttt	ctc	aac	ttc	aat	gcc	tat	gtg	gtg	ggc	gaa	atc	gcg	tac	ttt	ata	144	
Phe	Leu	Asn	Phe	Asn	Ala	Tyr	Val	Val	Gly	Glu	Ile	Ala	Tyr	Phe	Ile		
		35					40					45					
gtc	cat	ata	atg	tcg	acg	act	act	ctt	ttg	gag	gcc	act	gca	gtg	gca	192	
Val	His	Ile	Met	Ser	Thr	Thr	Thr	Leu	Leu	Glu	Ala	Thr	Ala	Val	Ala		
	50					55				60							
ccg	tgc	att	ggt	ttc	agc	ttc	atg	gcc	gac	ttt	aag	cag	ttc	ggt	ctc	240	
Pro	Cys	Ile	Gly	Phe	Ser	Phe	Met	Ala	Asp	Phe	Lys	Gln	Phe	Gly	Leu		
65					70				75					80			
aca	gtg	aat	aga	aag	cga	ttg	gtc	aga	ttg	ctg	gat	gat	ctc	aag	gag	288	
Thr	Val	Asn	Arg	Lys	Arg	Leu	Val	Arg	Leu	Leu	Asp	Asp	Leu	Lys	Glu		
				85				90						95			
ata	ttt	cct	tta	gat	tta	gaa	gcg	cag	cgg	aag	tat	aac	gta	tcg	ttt	336	
Ile	Phe	Pro	Leu	Asp	Leu	Glu	Ala	Gln	Arg	Lys	Tyr	Asn	Val	Ser	Phe		
			100					105					110				
tac	cgg	aaa	cac	atg	aac	agg	gtc	atg	acc	cta	ttc	acc	atc	ctc	tgc	384	
Tyr	Arg	Lys	His	Met	Asn	Arg	Val	Met	Thr	Leu	Phe	Thr	Ile	Leu	Cys		
		115					120					125					
atg	acc	tac	acc	tcg	tca	ttt	agc	ttt	tat	cca	gcc	atc	aag	tcg	acc	432	
Met	Thr	Tyr	Thr	Ser	Ser	Phe	Ser	Phe	Tyr	Pro	Ala	Ile	Lys	Ser	Thr		
	130					135					140						
ata	aag	tat	tac	ctt	atg	gga	tcg	gaa	atc	ttt	gag	cgc	aac	tac	gga	480	
Ile	Lys	Tyr	Tyr	Leu	Met	Gly	Ser	Glu	Ile	Phe	Glu	Arg	Asn	Tyr	Gly		
145					150				155					160			
ttt	cac	att	ttg	ttt	ccc	tac	gac	gca	gaa	acg	gat	ctg	acg	gtc	tac	528	
Phe	His	Ile	Leu	Phe	Pro	Tyr	Asp	Ala	Glu	Thr	Asp	Leu	Thr	Val	Tyr		
			165					170					175				
tgg	ttt	tcc	tac	tgg	gga	ttg	gct	cat	tgt	gcc	tat	gtg	gcc	gga	gtt	576	
Trp	Phe	Ser	Tyr	Trp	Gly	Leu	Ala	His	Cys	Ala	Tyr	Val	Ala	Gly	Val		
			180					185					190				
tcc	tac	gtc	tgc	gtg	gat	ctc	ctg	ctg	atc	gcg	acc	ata	acc	cag	ctg	624	

Ser Tyr Val Cys Val Asp Leu Leu Leu Ile Ala Thr Ile Thr Gln Leu	
195	200 205
acc atg cac ttc aac ttt ata gcg aat gat ttg gag gcc tac gaa gga	672
Thr Met His Phe Asn Phe Ile Ala Asn Asp Leu Glu Ala Tyr Glu Gly	
210	215 220
ggt gat cat acg gat gaa gaa aat atc aaa tac ctg cac aac ttg gtc	720
Gly Asp His Thr Asp Glu Glu Asn Ile Lys Tyr Leu His Asn Leu Val	
225	230 235 240
gtc tat cat gcc agg gcg ctg gac ctc agc gag gag gtc aac aac ata	768
Val Tyr His Ala Arg Ala Leu Asp Leu Ser Glu Glu Val Asn Asn Ile	
	245 250 255
ttc agc ttc ctg atc ctg tgg aac ttt att gcc gca tcg ctc gtg att	816
Phe Ser Phe Leu Ile Leu Trp Asn Phe Ile Ala Ala Ser Leu Val Ile	
	260 265 270
tgc ttc gct ggc ttt cag att aca gcc tca aat gtg gag gac ata ggg	864
Cys Phe Ala Gly Phe Gln Ile Thr Ala Ser Asn Val Glu Asp Ile Gly	
	275 280 285
gtg tac ttc ata ttt ttt tca gct tcg ctg gtt caa gtc ttt aaa tgt	912
Val Tyr Phe Ile Phe Phe Ser Ala Ser Leu Val Gln Val Phe Lys Cys	
	290 295 300
tct ttt cag agc tct cgg att ggc cat tcg gca ttt aat cag aac tgg	960
Ser Phe Gln Ser Ser Arg Ile Gly His Ser Ala Phe Asn Gln Asn Trp	
305	310 315 320
ttg cca tgc agc acc aaa tac aaa cgc atc ctg cag ttt att atc gcg	1008
Leu Pro Cys Ser Thr Lys Tyr Lys Arg Ile Leu Gln Phe Ile Ile Ala	
	325 330 335
cgc agc cag aag ccc gcc tct ata aga ccg cct acc ttt cca ccc ata	1056
Arg Ser Gln Lys Pro Ala Ser Ile Arg Pro Pro Thr Phe Pro Pro Ile	
	340 345 350
tct ttt aat acc ttt atg aag gta atc agc atg tcg tat cag ttt ttt	1104
Ser Phe Asn Thr Phe Met Lys Val Ile Ser Met Ser Tyr Gln Phe Phe	
	355 360 365
gca ctg ctc cgc acc aca tat tat ggt	1131
Ala Leu Leu Arg Thr Thr Tyr Tyr Gly	
	370 375

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<211> 377

<212> PRT

<213> *Drosophila melanogaster*

<400> 58

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Pro Asn Val Ile Arg Arg Tyr Leu Leu Arg Phe Tyr Leu Val Leu Gly
20 25 30

Phe Leu Asn Phe Asn Ala Tyr Val Val Gly Glu Ile Ala Tyr Phe Ile
35 40 45

Val His Ile Met Ser Thr Thr Thr Leu Leu Glu Ala Thr Ala Val Ala
50 55 60

Pro Cys Ile Gly Phe Ser Phe Met Ala Asp Phe Lys Gln Phe Gly Leu
65 70 75 80

Thr Val Asn Arg Lys Arg Leu Val Arg Leu Leu Asp Asp Leu Lys Glu
85 90 95

Ile Phe Pro Leu Asp Leu Glu Ala Gln Arg Lys Tyr Asn Val Ser Phe
100 105 110

Tyr Arg Lys His Met Asn Arg Val Met Thr Leu Phe Thr Ile Leu Cys
115 120 125

Met Thr Tyr Thr Ser Ser Phe Ser Phe Tyr Pro Ala Ile Lys Ser Thr
130 135 140

Ile Lys Tyr Tyr Leu Met Gly Ser Glu Ile Phe Glu Arg Asn Tyr Gly
145 150 155 160

Phe His Ile Leu Phe Pro Tyr Asp Ala Glu Thr Asp Leu Thr Val Tyr
165 170 175

Trp Phe Ser Tyr Trp Gly Leu Ala His Cys Ala Tyr Val Ala Gly Val
180 185 190

Ser Tyr Val Cys Val Asp Leu Leu Leu Ile Ala Thr Ile Thr Gln Leu
195 200 205

Thr Met His Phe Asn Phe Ile Ala Asn Asp Leu Glu Ala Tyr Glu Gly
210 215 220

Gly Asp His Thr Asp Glu Glu Asn Ile Lys Tyr Leu His Asn Leu Val
 225 230 235 240

Val Tyr His Ala Arg Ala Leu Asp Leu Ser Glu Glu Val Asn Asn Ile
 245 250 255

Phe Ser Phe Leu Ile Leu Trp Asn Phe Ile Ala Ala Ser Leu Val Ile
 260 265 270

Cys Phe Ala Gly Phe Gln Ile Thr Ala Ser Asn Val Glu Asp Ile Gly
 275 280 285

Val Tyr Phe Ile Phe Phe Ser Ala Ser Leu Val Gln Val Phe Lys Cys
 290 295 300

Ser Phe Gln Ser Ser Arg Ile Gly His Ser Ala Phe Asn Gln Asn Trp
 305 310 315 320

Leu Pro Cys Ser Thr Lys Tyr Lys Arg Ile Leu Gln Phe Ile Ile Ala
 325 330 335

Arg Ser Gln Lys Pro Ala Ser Ile Arg Pro Pro Thr Phe Pro Pro Ile
 340 345 350

Ser Phe Asn Thr Phe Met Lys Val Ile Ser Met Ser Tyr Gln Phe Phe
 355 360 365

Ala Leu Leu Arg Thr Thr Tyr Tyr Gly
 370 375

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 <223> DOR 94D.1

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gtc atg caa cta ttt ggc ctc tgg ccg tgg tcc ttg aaa tcg gaa gag 96

Val Met Gln Leu Phe Gly Leu Trp Pro Trp Ser Leu Lys Ser Glu Glu	
20 25 30	
gag tgg act ttc acc ggt ttt gta aag cgc aac tat cgc ttc ctg ctc	144
Glu Trp Thr Phe Thr Gly Phe Val Lys Arg Asn Tyr Arg Phe Leu Leu	
35 40 45	
cat ctg ccc att acc ttc acc ttt att gga ctc atg tgg ctg gag gcc	192
His Leu Pro Ile Thr Phe Thr Phe Ile Gly Leu Met Trp Leu Glu Ala	
50 55 60	
ttc atc tcg agc aat ctg gag cag gct ggc cag gtt ctg tac atg tcc	240
Phe Ile Ser Ser Asn Leu Glu Gln Ala Gly Gln Val Leu Tyr Met Ser	
65 70 75 80	
atc acc gag atg gct ttg gtg gtg aaa atc ctg agc att tgg cac tat	288
Ile Thr Glu Met Ala Leu Val Val Lys Ile Leu Ser Ile Trp His Tyr	
85 90 95	
cgc acc gaa gct tgg cgg ctg atg tac gaa ctc caa cat gct ccg gac	336
Arg Thr Glu Ala Trp Arg Leu Met Tyr Glu Leu Gln His Ala Pro Asp	
100 105 110	
tac caa ctc cac aac cag gag gag gta gac ttt tgg cgc cgg gag caa	384
Tyr Gln Leu His Asn Gln Glu Glu Val Asp Phe Trp Arg Arg Glu Gln	
115 120 125	
cga ttc ttc aag tgg ttc ttc tac atc tac att ctg att agc ttg ggc	432
Arg Phe Phe Lys Trp Phe Phe Tyr Ile Tyr Ile Leu Ile Ser Leu Gly	
130 135 140	
gtg gta tat agt ggc tgc act gga gta ctt ttt ctg gag ggc tac gaa	480
Val Val Tyr Ser Gly Cys Thr Gly Val Leu Phe Leu Glu Gly Tyr Glu	
145 150 155 160	
ctg ccc ttt gcc tac tac gtg ccc ttc gaa tgg cag aac gag aga agg	528
Leu Pro Phe Ala Tyr Tyr Val Pro Phe Glu Trp Gln Asn Glu Arg Arg	
165 170 175	
tac tgg ttc gcc tat ggt tac gat atg gcg ggc atg acg ctg acc tgc	576
Tyr Trp Phe Ala Tyr Gly Tyr Asp Met Ala Gly Met Thr Leu Thr Cys	
180 185 190	
atc tca aac att acc ctg gac acc ctg ggt tgc tat ttc ctg ttc cat	624
Ile Ser Asn Ile Thr Leu Asp Thr Leu Gly Cys Tyr Phe Leu Phe His	
195 200 205	
atc tct ctt ttg tac cga ctg ctt ggt ctg cga ttg agg gaa acg aag	672

Ile Ser Leu Leu Tyr Arg Leu Leu Gly Leu Arg Leu Arg Glu Thr Lys	
210	215 220
aat atg aag aat gat acc att ttt ggc cag cag ttg cgt gcc atc ttc	720
Asn Met Lys Asn Asp Thr Ile Phe Gly Gln Gln Leu Arg Ala Ile Phe	
225	230 235 240
att atg cat cag agg att aga agc cta acc ctg acc tgc cag aga atc	768
Ile Met His Gln Arg Ile Arg Ser Leu Thr Leu Thr Cys Gln Arg Ile	
	245 250 255
gta tct ccc tat atc cta tct cag atc att ttg agt gcc ctg atc atc	816
Val Ser Pro Tyr Ile Leu Ser Gln Ile Ile Leu Ser Ala Leu Ile Ile	
	260 265 270
tgc ttt agt gga tac cgc ttg cag cat gtg gga att cgc gat aat ccc	864
Cys Phe Ser Gly Tyr Arg Leu Gln His Val Gly Ile Arg Asp Asn Pro	
	275 280 285
ggc cag ttt ata tcc atg ttg cag ttt gtc agt gtg atg atc ctg cag	912
Gly Gln Phe Ile Ser Met Leu Gln Phe Val Ser Val Met Ile Leu Gln	
	290 295 300
att tac ttg ccc tgc tac tat gga aac gag ata acc gtg tat gcc aat	960
Ile Tyr Leu Pro Cys Tyr Tyr Gly Asn Glu Ile Thr Val Tyr Ala Asn	
305	310 315 320
cag ctg acc aac gag gtt tac cat acc aat tgg ctg gaa tgt cgg cca	1008
Gln Leu Thr Asn Glu Val Tyr His Thr Asn Trp Leu Glu Cys Arg Pro	
	325 330 335
ccg att cga aag tta ctc aat gcc tac atg gag cac ctg aag aaa ccg	1056
Pro Ile Arg Lys Leu Leu Asn Ala Tyr Met Glu His Leu Lys Lys Pro	
	340 345 350
gtg acc atc cgg gct ggc aac tac ttc gcc gtg gga cta cca att ttt	1104
Val Thr Ile Arg Ala Gly Asn Tyr Phe Ala Val Gly Leu Pro Ile Phe	
	355 360 365
gtt aag acc atc aac aac gcc tac agt ttc ttg gct tta tta cta aat	1152
Val Lys Thr Ile Asn Asn Ala Tyr Ser Phe Leu Ala Leu Leu Leu Asn	
	370 375 380
gta tcg aat	1161
Val Ser Asn	
385	

<213> Drosophila melanogaster

Met Asp Lys His Lys Asp Arg Ile Glu Ser Met Arg Leu Ile Leu Gln
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Val Met Gln Leu Phe Gly Leu Trp Pro Trp Ser Leu Lys Ser Glu Glu
20 25 30

Glu Trp Thr Phe Thr Gly Phe Val Lys Arg Asn Tyr Arg Phe Leu Leu
35 40 45

His Leu Pro Ile Thr Phe Thr Phe Ile Gly Leu Met Trp Leu Glu Ala
50 55 60

Phe Ile Ser Ser Asn Leu Glu Gln Ala Gly Gln Val Leu Tyr Met Ser
65 70 75 80

Ile Thr Glu Met Ala Leu Val Val Lys Ile Leu Ser Ile Trp His Tyr
85 90 95

Arg Thr Glu Ala Trp Arg Leu Met Tyr Glu Leu Gln His Ala Pro Asp
100 105 110

Tyr Gln Leu His Asn Gln Glu Glu Val Asp Phe Trp Arg Arg Glu Gln
115 120 125

Arg Phe Phe Lys Trp Phe Phe Tyr Ile Tyr Ile Leu Ile Ser Leu Gly
130 135 140

Val	Val	Tyr	Ser	Gly	Cys	Thr	Gly	Val	Leu	Phe	Leu	Glu	Gly	Tyr	Glu
145					150					155					160

Leu Pro Phe Ala Tyr Tyr Val Pro Phe Glu Trp Gln Asn Glu Arg Arg
165 170 175

Tyr Trp Phe Ala Tyr Gly Tyr Asp Met Ala Gly Met Thr Leu Thr Cys
180 185 190

Ile Ser Asn Ile Thr Leu Asp Thr Leu Gly Cys Tyr Phe Leu Phe His
195 200 205

Ile Ser Leu Leu Tyr Arg Leu Leu Gly Leu Arg Leu Arg Glu Thr Lys
210 215 220

Asn Met Lys Asn Asp Thr Ile Phe Gly Gln Gln Leu Arg Ala Ile Phe
 225 230 235 240

Ile Met His Gln Arg Ile Arg Ser Leu Thr Leu Thr Cys Gln Arg Ile
 245 250 255

Val Ser Pro Tyr Ile Leu Ser Gln Ile Ile Leu Ser Ala Leu Ile Ile
 260 265 270

Cys Phe Ser Gly Tyr Arg Leu Gln His Val Gly Ile Arg Asp Asn Pro
 275 280 285

Gly Gln Phe Ile Ser Met Leu Gln Phe Val Ser Val Met Ile Leu Gln
 290 295 300

Ile Tyr Leu Pro Cys Tyr Tyr Gly Asn Glu Ile Thr Val Tyr Ala Asn
 305 310 315 320

Gln Leu Thr Asn Glu Val Tyr His Thr Asn Trp Leu Glu Cys Arg Pro
 325 330 335

Pro Ile Arg Lys Leu Leu Asn Ala Tyr Met Glu His Leu Lys Lys Pro
 340 345 350

Val Thr Ile Arg Ala Gly Asn Tyr Phe Ala Val Gly Leu Pro Ile Phe
 355 360 365

Val Lys Thr Ile Asn Asn Ala Tyr Ser Phe Leu Ala Leu Leu Leu Asn
 370 375 380

Val Ser Asn
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 <211> 1101
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 <213> *Drosophila melanogaster*

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caa cgt tgg ata gga ctt ctt aaa tgg gaa aac gag ggc gag gat gga	96
Gln Arg Trp Ile Gly Leu Leu Lys Trp Glu Asn Glu Gly Glu Asp Gly	
20 25 30	
gta tta acc tgg cta aaa cga ata tat cct ttt gta ctg cac ctt cca	144
Val Leu Thr Trp Leu Lys Arg Ile Tyr Pro Phe Val Leu His Leu Pro	
35 40 45	
ctg acc ttc acg tat att gcc tta atg tgg tat gaa gct att aca tcg	192
Leu Thr Phe Thr Tyr Ile Ala Leu Met Trp Tyr Glu Ala Ile Thr Ser	
50 55 60	
tca gat ttt gag gaa gct ggt caa gtt ctg tac atg tcc atc acc gaa	240
Ser Asp Phe Glu Glu Ala Gly Gln Val Leu Tyr Met Ser Ile Thr Glu	
65 70 75 80	
ctg gca ttg gtc act aaa ctg ctg aat att tgg tat cgt cgt cat gaa	288
Leu Ala Leu Val Thr Lys Leu Leu Asn Ile Trp Tyr Arg Arg His Glu	
85 90 95	
gct gct agt cta atc cac gaa ttg caa cac gat ccc gca ttt aat ctg	336
Ala Ala Ser Leu Ile His Glu Leu Gln His Asp Pro Ala Phe Asn Leu	
100 105 110	
cgc aat tcg gag gaa atc aaa ttc tgg cag caa aat cag agg aac ttt	384
Arg Asn Ser Glu Glu Ile Lys Phe Trp Gln Gln Asn Gln Arg Asn Phe	
115 120 125	
aag aga ata ttt tac tgg tac atc tgg ggc agc ctt ttc gtg gct gta	432
Lys Arg Ile Phe Tyr Trp Tyr Ile Trp Gly Ser Leu Phe Val Ala Val	
130 135 140	
atg ggt tat ata agc gtg ttt ttc cag gag gat tac gag ctg ccc ttt	480
Met Gly Tyr Ile Ser Val Phe Phe Gln Glu Asp Tyr Glu Leu Pro Phe	
145 150 155 160	
ggc tac tac gtg cca ttc gag tgg cgc acc agg gaa cga tac ttc tac	528
Gly Tyr Tyr Val Pro Phe Glu Trp Arg Thr Arg Glu Arg Tyr Phe Tyr	
165 170 175	
gct tgg ggc tat aat gtg gtg gcc atg acc ctg tgc tgt cta tcc aac	576
Ala Trp Gly Tyr Asn Val Val Ala Met Thr Leu Cys Cys Leu Ser Asn	
180 185 190	
atc cta ctg gac aca cta ggc tgt tat ttc atg ttc cac atc gcc tcg	624
Ile Leu Leu Asp Thr Leu Gly Cys Tyr Phe Met Phe His Ile Ala Ser	
195 200 205	

ctt ttc agg ctt ttg gga atg cga ctg gag gcc ttg aaa aat gca gcc	672
Leu Phe Arg Leu Leu Gly Met Arg Leu Glu Ala Leu Lys Asn Ala Ala	
210 215 220	
gaa gag aaa gcc aga ccg gag ttg cgc cgc att ttc caa ctg cac act	720
Glu Glu Lys Ala Arg Pro Glu Leu Arg Arg Ile Phe Gln Leu His Thr	
225 230 235 240	
aaa gtc cgc cga ttg acg agg gaa tgc gaa gtg tta gtt tca ccc tat	768
Lys Val Arg Arg Leu Thr Arg Glu Cys Glu Val Leu Val Ser Pro Tyr	
245 250 255	
gtt cta tcc caa gtg gtc ttc agt gcc ttc atc atc tgc ttc agt gcc	816
Val Leu Ser Gln Val Val Phe Ser Ala Phe Ile Ile Cys Phe Ser Ala	
260 265 270	
tat cga ctg gtg cac atg ggc ttc aag cag cga cct gga ctc ttc gtg	864
Tyr Arg Leu Val His Met Gly Phe Lys Gln Arg Pro Gly Leu Phe Val	
275 280 285	
acc acc gtg caa ttc gtg gcc gtc atg atc gtc cag att ttc ttg ccc	912
Thr Thr Val Gln Phe Val Ala Val Met Ile Val Gln Ile Phe Leu Pro	
290 295 300	
tgt tac tac ggc aat gag ttg acc ttt cat gcc aat gca ctc act aat	960
Cys Tyr Tyr Gly Asn Glu Leu Thr Phe His Ala Asn Ala Leu Thr Asn	
305 310 315 320	
agt gtc ttc ggt acc aat tgg ctg gag tac tcc gtg ggc act cgc aag	1008
Ser Val Phe Gly Thr Asn Trp Leu Glu Tyr Ser Val Gly Thr Arg Lys	
325 330 335	
ctg ctt aac tgc tac atg gag ttc ctc aag cga ccg gtt aaa acc atc	1056
Leu Leu Asn Cys Tyr Met Glu Phe Leu Lys Arg Pro Val Lys Thr Ile	
340 345 350	
aac aat gcc tac agt ttc ttc gcc ctg ctg cta aag ata tcc aag	1101
Asn Asn Ala Tyr Ser Phe Phe Ala Leu Leu Leu Lys Ile Ser Lys	
355 360 365	

<210> 62

<211> 367

<212> PRT

<213> *Drosophila melanogaster*

<400> 62

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Gln	Arg	Trp	Ile	Gly	Leu	Leu	Lys	Trp	Glu	Asn	Glu	Gly	Glu	Asp	Gly	20	25	30	
Val	Leu	Thr	Trp	Leu	Lys	Arg	Ile	Tyr	Pro	Phe	Val	Leu	His	Leu	Pro	35	40	45	
Leu	Thr	Phe	Thr	Tyr	Ile	Ala	Leu	Met	Trp	Tyr	Glu	Ala	Ile	Thr	Ser	50	55	60	
Ser	Asp	Phe	Glu	Glu	Ala	Gly	Gln	Val	Leu	Tyr	Met	Ser	Ile	Thr	Glu	65	70	75	80
Leu	Ala	Leu	Val	Thr	Lys	Leu	Leu	Asn	Ile	Trp	Tyr	Arg	Arg	His	Glu	85	90	95	
Ala	Ala	Ser	Leu	Ile	His	Glu	Leu	Gln	His	Asp	Pro	Ala	Phe	Asn	Leu	100	105	110	
Arg	Asn	Ser	Glu	Glu	Ile	Lys	Phe	Trp	Gln	Gln	Asn	Gln	Arg	Asn	Phe	115	120	125	
Lys	Arg	Ile	Phe	Tyr	Trp	Tyr	Ile	Trp	Gly	Ser	Leu	Phe	Val	Ala	Val	130	135	140	
Met	Gly	Tyr	Ile	Ser	Val	Phe	Phe	Gln	Glu	Asp	Tyr	Glu	Leu	Pro	Phe	145	150	155	160
Gly	Tyr	Tyr	Val	Pro	Phe	Glu	Trp	Arg	Thr	Arg	Glu	Arg	Tyr	Phe	Tyr	165	170	175	
Ala	Trp	Gly	Tyr	Asn	Val	Val	Ala	Met	Thr	Leu	Cys	Cys	Leu	Ser	Asn	180	185	190	
Ile	Leu	Leu	Asp	Thr	Leu	Gly	Cys	Tyr	Phe	Met	Phe	His	Ile	Ala	Ser	195	200	205	
Leu	Phe	Arg	Leu	Leu	Gly	Met	Arg	Leu	Glu	Ala	Leu	Lys	Asn	Ala	Ala	210	215	220	
Glu	Glu	Lys	Ala	Arg	Pro	Glu	Leu	Arg	Arg	Ile	Phe	Gln	Leu	His	Thr	225	230	235	240
Lys	Val	Arg	Arg	Leu	Thr	Arg	Glu	Cys	Glu	Val	Leu	Val	Ser	Pro	Tyr	245	250	255	

Val Leu Ser Gln Val Val Phe Ser Ala Phe Ile Ile Cys Phe Ser Ala
 260 265 270
 Tyr Arg Leu Val His Met Gly Phe Lys Gln Arg Pro Gly Leu Phe Val
 275 280 285
 Thr Thr Val Gln Phe Val Ala Val Met Ile Val Gln Ile Phe Leu Pro
 290 295 300
 Cys Tyr Tyr Gly Asn Glu Leu Thr Phe His Ala Asn Ala Leu Thr Asn
 305 310 315 320
 Ser Val Phe Gly Thr Asn Trp Leu Glu Tyr Ser Val Gly Thr Arg Lys
 325 330 335
 Leu Leu Asn Cys Tyr Met Glu Phe Leu Lys Arg Pro Val Lys Thr Ile
 340 345 350
 Asn Asn Ala Tyr Ser Phe Phe Ala Leu Leu Leu Lys Ile Ser Lys
 355 360 365

<210> 63
 <211> 1095
 <212> DNA
 <213> *Drosophila melanogaster*

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 <222> (1)..(1095)
 <223> DORLU 1.1

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 gtg tat ctc ttc tgg acc tgc gtg ccc ttc gcc ttc ggg gtg ttt tac 96
 Val Tyr Leu Phe Trp Thr Cys Val Pro Phe Ala Phe Gly Val Phe Tyr
 20 25 30
 ctg ccc gtg ggc ttc atc atc agc tac gtg cag gag ttc aag aac ttc 144
 Leu Pro Val Gly Phe Ile Ile Ser Tyr Val Gln Glu Phe Lys Asn Phe
 35 40 45
 acg ccg ggc gag ttc ctt acc tcg ctg cag gtg tgc atc aat gtg tat 192
 Thr Pro Gly Glu Phe Leu Thr Ser Leu Gln Val Cys Ile Asn Val Tyr

50	55	60	
ggc gcc tcg gtg aag tcc acc atc acc tac ctc ttc ctc tgg cga ctg			240
Gly Ala Ser Val Lys Ser Thr Ile Thr Tyr Leu Phe Leu Trp Arg Leu			
65	70	75	80
cgc aag acg gag atc ctt ctg gac tcc ctg gac aag agg ctg gcg aac			288
Arg Lys Thr Glu Ile Leu Leu Asp Ser Leu Asp Lys Arg Leu Ala Asn			
	85	90	95
gac agc gat cgc gag agg atc cac aat atg gtg gcg cgc tgc aac tac			336
Asp Ser Asp Arg Glu Arg Ile His Asn Met Val Ala Arg Cys Asn Tyr			
	100	105	110
gcc ttt ctc atc tac agc ttc atc tac tgc gga tac gcg ggt tcc act			384
Ala Phe Leu Ile Tyr Ser Phe Ile Tyr Cys Gly Tyr Ala Gly Ser Thr			
	115	120	125
ttc ctg tcc tac gcc ctc agt ggt cgt cct ccg tgg tcc gtc tac aat			432
Phe Leu Ser Tyr Ala Leu Ser Gly Arg Pro Pro Trp Ser Val Tyr Asn			
	130	135	140
ccc ttc atc gat tgg cgc gat ggc atg ggc agc ctg tgg atc cag gcc			480
Pro Phe Ile Asp Trp Arg Asp Gly Met Gly Ser Leu Trp Ile Gln Ala			
145	150	155	160
ata ttc gag tac atc acc atg tcc ttc gcc gtg ctg cag gac cag cta			528
Ile Phe Glu Tyr Ile Thr Met Ser Phe Ala Val Leu Gln Asp Gln Leu			
	165	170	175
tcc gac acg tat ccc ctg atg ttc acc att atg ttc cgg gcc cac atg			576
Ser Asp Thr Tyr Pro Leu Met Phe Thr Ile Met Phe Arg Ala His Met			
	180	185	190
gag gtc ctc aag gat cac gtg cgg agc ctg cgc atg gat ccc gag cgc			624
Glu Val Leu Lys Asp His Val Arg Ser Leu Arg Met Asp Pro Glu Arg			
	195	200	205
agt gag gca gac aac tat cag gat ctg gtg aac tgc gtg ctg gac cac			672
Ser Glu Ala Asp Asn Tyr Gln Asp Leu Val Asn Cys Val Leu Asp His			
	210	215	220
aag act ata ctg aaa tgc tgt gac atg att cgc ccc atg ata tcc cgc			720
Lys Thr Ile Leu Lys Cys Cys Asp Met Ile Arg Pro Met Ile Ser Arg			
225	230	235	240
acc atc ttc gtg caa ttc gcg ctg att ggt tcc gtt ttg ggc ctg acc			768
Thr Ile Phe Val Gln Phe Ala Leu Ile Gly Ser Val Leu Gly Leu Thr			

245	250	255	
ctg gtg aac gtg ttc ttc ttc tcg aac ttc tgg aag ggc gtg gcc tcg			816
Leu Val Asn Val Phe Phe Phe Ser Asn Phe Trp Lys Gly Val Ala Ser			
260	265	270	
ctc ctg ttc gtc atc acc atc ctg ctg cag acc ttc ccg ttc tgc tac			864
Leu Leu Phe Val Ile Thr Ile Leu Leu Gln Thr Phe Pro Phe Cys Tyr			
275	280	285	
acc tgc aac atg ctg atc gac gat gcc cag gat ctg tcc aac gag att			912
Thr Cys Asn Met Leu Ile Asp Asp Ala Gln Asp Leu Ser Asn Glu Ile			
290	295	300	
ttc cag tcc aac tgg gtg gac gcg gag ccg cgc tac aag gcg acg ctg			960
Phe Gln Ser Asn Trp Val Asp Ala Glu Pro Arg Tyr Lys Ala Thr Leu			
305	310	315	320
gtg ctc ttc atg cac cat gtt cag cag ccc ata atc ttc att gcc gga			1008
Val Leu Phe Met His His Val Gln Gln Pro Ile Ile Phe Ile Ala Gly			
325	330	335	
ggc atc ttt ccc atc tct atg aac agc aac ata acc gta agg att act			1056
Gly Ile Phe Pro Ile Ser Met Asn Ser Asn Ile Thr Val Arg Ile Thr			
340	345	350	
tct ttc ctg cca act gcc tac ttc aca ttt gac cca ttt			1095
Ser Phe Leu Pro Thr Ala Tyr Phe Thr Phe Asp Pro Phe			
355	360	365	

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<211> 365

<212> PRT

<213> Drosophila melanogaster

<400> 64

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Val Tyr Leu Phe Trp Thr Cys Val Pro Phe Ala Phe Gly Val Phe Tyr
20 25 30

Leu Pro Val Gly Phe Ile Ile Ser Tyr Val Gln Glu Phe Lys Asn Phe
35 40 45

Thr Pro Gly Glu Phe Leu Thr Ser Leu Gln Val Cys Ile Asn Val Tyr
50 55 60

Gly	Ala	Ser	Val	Lys	Ser	Thr	Ile	Thr	Tyr	Leu	Phe	Leu	Trp	Arg	Leu		
65					70					75					80		
Arg	Lys	Thr	Glu	Ile	Leu	Leu	Asp	Ser	Leu	Asp	Lys	Arg	Leu	Ala	Asn		
				85					90						95		
Asp	Ser	Asp	Arg	Glu	Arg	Ile	His	Asn	Met	Val	Ala	Arg	Cys	Asn	Tyr		
				100				105						110			
Ala	Phe	Leu	Ile	Tyr	Ser	Phe	Ile	Tyr	Cys	Gly	Tyr	Ala	Gly	Ser	Thr		
				115				120						125			
Phe	Leu	Ser	Tyr	Ala	Leu	Ser	Gly	Arg	Pro	Pro	Trp	Ser	Val	Tyr	Asn		
				130				135						140			
Pro	Phe	Ile	Asp	Trp	Arg	Asp	Gly	Met	Gly	Ser	Leu	Trp	Ile	Gln	Ala		
145						150				155					160		
Ile	Phe	Glu	Tyr	Ile	Thr	Met	Ser	Phe	Ala	Val	Leu	Gln	Asp	Gln	Leu		
					165				170					175			
Ser	Asp	Thr	Tyr	Pro	Leu	Met	Phe	Thr	Ile	Met	Phe	Arg	Ala	His	Met		
				180					185					190			
Glu	Val	Leu	Lys	Asp	His	Val	Arg	Ser	Leu	Arg	Met	Asp	Pro	Glu	Arg		
				195				200					205				
Ser	Glu	Ala	Asp	Asn	Tyr	Gln	Asp	Leu	Val	Asn	Cys	Val	Leu	Asp	His		
				210				215				220					
Lys	Thr	Ile	Leu	Lys	Cys	Cys	Asp	Met	Ile	Arg	Pro	Met	Ile	Ser	Arg		
225						230				235					240		
Thr	Ile	Phe	Val	Gln	Phe	Ala	Leu	Ile	Gly	Ser	Val	Leu	Gly	Leu	Thr		
					245				250					255			
Leu	Val	Asn	Val	Phe	Phe	Phe	Ser	Asn	Phe	Trp	Lys	Gly	Val	Ala	Ser		
					260				265					270			
Leu	Leu	Phe	Val	Ile	Thr	Ile	Leu	Leu	Gln	Thr	Phe	Pro	Phe	Cys	Tyr		
					275				280					285			
Thr	Cys	Asn	Met	Leu	Ile	Asp	Asp	Ala	Gln	Asp	Leu	Ser	Asn	Glu	Ile		
					290			295				300					
Phe	Gln	Ser	Asn	Trp	Val	Asp	Ala	Glu	Pro	Arg	Tyr	Lys	Ala	Thr	Leu		
305						310				315					320		

Val Leu Phe Met His His Val Gln Gln Pro Ile Ile Phe Ile Ala Gly
 325 330 335

Gly Ile Phe Pro Ile Ser Met Asn Ser Asn Ile Thr Val Arg Ile Thr
 340 345 350

Ser Phe Leu Pro Thr Ala Tyr Phe Thr Phe Asp Pro Phe
 355 360 365

<210> 65

<211> 1233

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1233)

<223> DORLU 2.1

<400> 65

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 Met Thr Lys Phe Phe Phe Lys Arg Leu Gln Thr Ala Pro Leu Asp Gln
 1 5 10 15

gag gtg agt tcc ctt gat gcc agc gac tac tac tac cgc atc gca ttt 96
 Glu Val Ser Ser Leu Asp Ala Ser Asp Tyr Tyr Tyr Arg Ile Ala Phe
 20 25 30

ttc ctg ggc tgg acc ccg ccc aag ggg gct ctg ctc cga tgg atc tac 144
 Phe Leu Gly Trp Thr Pro Pro Lys Gly Ala Leu Leu Arg Trp Ile Tyr
 35 40 45

tcc ctg tgg act ctg acc acg atg tgg ctg ggt atc gtg tac ctg ccg 192
 Ser Leu Trp Thr Leu Thr Thr Met Trp Leu Gly Ile Val Tyr Leu Pro
 50 55 60

ctc gga ctg agc ctc acc tat gtg aag cac ttc gat aga ttc acg ccg 240
 Leu Gly Leu Ser Leu Thr Tyr Val Lys His Phe Asp Arg Phe Thr Pro
 65 70 75 80

acg gag ttc ctg acc tcc ctg cag gtg gat atc aac tgc atc ggg aac 288
 Thr Glu Phe Leu Thr Ser Leu Gln Val Asp Ile Asn Cys Ile Gly Asn
 85 90 95

gtg atc aag tca tgc gta act tat tcc cag atg tgg cgt ttt cgc cgg 336

Val	Ile	Lys	Ser	Cys	Val	Thr	Tyr	Ser	Gln	Met	Trp	Arg	Phe	Arg	Arg		
			100					105					110				
atg	aat	gag	ctt	atc	tcg	tcc	ctg	gac	aag	aga	tgt	gtg	act	acg	aca	384	
Met	Asn	Glu	Leu	Ile	Ser	Ser	Leu	Asp	Lys	Arg	Cys	Val	Thr	Thr	Thr		
		115					120				125						
cag	cgt	cga	att	ttc	cat	aag	atg	gtg	gca	cgg	gtt	aat	ctc	atc	gtg	432	
Gln	Arg	Arg	Ile	Phe	His	Lys	Met	Val	Ala	Arg	Val	Asn	Leu	Ile	Val		
	130					135				140							
att	ctg	ttc	ttg	tcc	acg	tac	ttg	ggc	ttc	tgc	ttt	cta	act	ctg	ttc	480	
Ile	Leu	Phe	Leu	Ser	Thr	Tyr	Leu	Gly	Phe	Cys	Phe	Leu	Thr	Leu	Phe		
145					150					155					160		
act	tcg	gtt	ttc	gct	ggc	aaa	gct	cct	tgg	cag	ctg	tac	aac	cca	ctg	528	
Thr	Ser	Val	Phe	Ala	Gly	Lys	Ala	Pro	Trp	Gln	Leu	Tyr	Asn	Pro	Leu		
			165					170					175				
gtg	gac	tgg	cgg	aaa	ggc	cat	tgg	cag	cta	tgg	att	gcc	tcc	atc	ctg	576	
Val	Asp	Trp	Arg	Lys	Gly	His	Trp	Gln	Leu	Trp	Ile	Ala	Ser	Ile	Leu		
		180						185					190				
gag	tac	tgt	gtg	gtc	tcc	att	ggc	acc	atg	cag	gag	ttg	atg	tcc	gac	624	
Glu	Tyr	Cys	Val	Val	Ser	Ile	Gly	Thr	Met	Gln	Glu	Leu	Met	Ser	Asp		
		195					200					205					
acc	tac	gcc	ata	gtg	ttc	atc	tcc	ttg	ttc	cgc	tgc	cac	ctg	gct	att	672	
Thr	Tyr	Ala	Ile	Val	Phe	Ile	Ser	Leu	Phe	Arg	Cys	His	Leu	Ala	Ile		
	210					215					220						
ctc	aga	gat	cgc	ata	gct	aat	ctg	cgg	cag	gat	ccg	aaa	ctc	agt	gag	720	
Leu	Arg	Asp	Arg	Ile	Ala	Asn	Leu	Arg	Gln	Asp	Pro	Lys	Leu	Ser	Glu		
225					230				235					240			
atg	gaa	cac	tat	gag	cag	atg	gtg	gcc	tgc	att	cag	gat	cat	cga	acc	768	
Met	Glu	His	Tyr	Glu	Gln	Met	Val	Ala	Cys	Ile	Gln	Asp	His	Arg	Thr		
		245						250					255				
atc	ata	cag	tgc	tcc	cag	att	att	cga	ccc	atc	ctg	tcg	atc	act	atc	816	
Ile	Ile	Gln	Cys	Ser	Gln	Ile	Ile	Arg	Pro	Ile	Leu	Ser	Ile	Thr	Ile		
		260						265					270				
ttt	gcc	cag	ttc	atg	ctg	gtt	ggc	att	gac	ttg	ggt	ctg	gcg	gcc	atc	864	
Phe	Ala	Gln	Phe	Met	Leu	Val	Gly	Ile	Asp	Leu	Gly	Leu	Ala	Ala	Ile		
		275					280					285					
agc	atc	ctc	ttc	ttt	ccg	aac	acc	att	tgg	acg	atc	atg	gca	aac	gtg	912	

Ser Ile Leu Phe Phe Pro Asn Thr Ile Trp Thr Ile Met Ala Asn Val
 290 295 300
 tcg ttc atc gtg gcc atc tgt aca gag tcc ttt cca tgc tgc atg ctc 960
 Ser Phe Ile Val Ala Ile Cys Thr Glu Ser Phe Pro Cys Cys Met Leu
 305 310 315 320
 tgc gag cat ctg atc gag gac tcc gtc cat gtg agc aac gcc ctg ttc 1008
 Cys Glu His Leu Ile Glu Asp Ser Val His Val Ser Asn Ala Leu Phe
 325 330 335
 cac tca aac tgg ata acc gcg gac agg agc tac aag tcg gcg gtt ctg 1056
 His Ser Asn Trp Ile Thr Ala Asp Arg Ser Tyr Lys Ser Ala Val Leu
 340 345 350
 tat ttc ctg cac cgg gct cag caa ccc att caa ttc acg gcc ggc tcc 1104
 Tyr Phe Leu His Arg Ala Gln Gln Pro Ile Gln Phe Thr Ala Gly Ser
 355 360 365
 ata ttt ccc att tcg gtg cag agc aac ata gcc gtg gcc aag ttc gcg 1152
 Ile Phe Pro Ile Ser Val Gln Ser Asn Ile Ala Val Ala Lys Phe Ala
 370 375 380
 ttc aca atc atc aca atc gtg aac caa atg aat ctg ggc gag aag ttc 1200
 Phe Thr Ile Ile Thr Ile Val Asn Gln Met Asn Leu Gly Glu Lys Phe
 385 390 395 400
 ttc agt gac agg agc aat ggc gat ata aat cct 1233
 Phe Ser Asp Arg Ser Asn Gly Asp Ile Asn Pro
 405 410

<210> 66
 <211> 411
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 66
 Met Thr Lys Phe Phe Phe Lys Arg Leu Gln Thr Ala Pro Leu Asp Gln
 1 5 10 15
 Glu Val Ser Ser Leu Asp Ala Ser Asp Tyr Tyr Tyr Arg Ile Ala Phe
 20 25 30
 Phe Leu Gly Trp Thr Pro Pro Lys Gly Ala Leu Leu Arg Trp Ile Tyr
 35 40 45
 Ser Leu Trp Thr Leu Thr Thr Met Trp Leu Gly Ile Val Tyr Leu Pro

50	55	60
Leu Gly Leu Ser Leu Thr Tyr Val Lys His Phe Asp Arg Phe Thr Pro		
65	70	75 80
Thr Glu Phe Leu Thr Ser Leu Gln Val Asp Ile Asn Cys Ile Gly Asn		
	85	90 95
Val Ile Lys Ser Cys Val Thr Tyr Ser Gln Met Trp Arg Phe Arg Arg		
	100	105 110
Met Asn Glu Leu Ile Ser Ser Leu Asp Lys Arg Cys Val Thr Thr Thr		
	115	120 125
Gln Arg Arg Ile Phe His Lys Met Val Ala Arg Val Asn Leu Ile Val		
	130	135 140
Ile Leu Phe Leu Ser Thr Tyr Leu Gly Phe Cys Phe Leu Thr Leu Phe		
145	150	155 160
Thr Ser Val Phe Ala Gly Lys Ala Pro Trp Gln Leu Tyr Asn Pro Leu		
	165	170 175
Val Asp Trp Arg Lys Gly His Trp Gln Leu Trp Ile Ala Ser Ile Leu		
	180	185 190
Glu Tyr Cys Val Val Ser Ile Gly Thr Met Gln Glu Leu Met Ser Asp		
	195	200 205
Thr Tyr Ala Ile Val Phe Ile Ser Leu Phe Arg Cys His Leu Ala Ile		
	210	215 220
Leu Arg Asp Arg Ile Ala Asn Leu Arg Gln Asp Pro Lys Leu Ser Glu		
225	230	235 240
Met Glu His Tyr Glu Gln Met Val Ala Cys Ile Gln Asp His Arg Thr		
	245	250 255
Ile Ile Gln Cys Ser Gln Ile Ile Arg Pro Ile Leu Ser Ile Thr Ile		
	260	265 270
Phe Ala Gln Phe Met Leu Val Gly Ile Asp Leu Gly Leu Ala Ala Ile		
	275	280 285
Ser Ile Leu Phe Phe Pro Asn Thr Ile Trp Thr Ile Met Ala Asn Val		
	290	295 300
Ser Phe Ile Val Ala Ile Cys Thr Glu Ser Phe Pro Cys Cys Met Leu		

305 310 315 320
 Cys Glu His Leu Ile Glu Asp Ser Val His Val Ser Asn Ala Leu Phe
 325 330 335
 His Ser Asn Trp Ile Thr Ala Asp Arg Ser Tyr Lys Ser Ala Val Leu
 340 345 350
 Tyr Phe Leu His Arg Ala Gln Gln Pro Ile Gln Phe Thr Ala Gly Ser
 355 360 365
 Ile Phe Pro Ile Ser Val Gln Ser Asn Ile Ala Val Ala Lys Phe Ala
 370 375 380
 Phe Thr Ile Ile Thr Ile Val Asn Gln Met Asn Leu Gly Glu Lys Phe
 385 390 395 400
 Phe Ser Asp Arg Ser Asn Gly Asp Ile Asn Pro
 405 410

<210> 67
 <211> 1191
 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <223> DORLU 4.1

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 1 5 10 15
 tcc cgg gat tcg ctg atc tac tta aac aga tcc ata gat caa atg gga 96
 Ser Arg Asp Ser Leu Ile Tyr Leu Asn Arg Ser Ile Asp Gln Met Gly
 20 25 30
 tgg aga ctg ccg cca cga act aag ccg tac tgg tgg ctc tat tac att 144
 Trp Arg Leu Pro Pro Arg Thr Lys Pro Tyr Trp Trp Leu Tyr Tyr Ile
 35 40 45
 tgg aca ttg gtg gtc ata gta ctc gtc ttt atc ttt ata ccc tat gga 192
 Trp Thr Leu Val Val Ile Val Leu Val Phe Ile Phe Ile Pro Tyr Gly
 50 55 60

ctg ata atg act gga ata aag gag ttc aag aac ttc acg acc acg gat	240
Leu Ile Met Thr Gly Ile Lys Glu Phe Lys Asn Phe Thr Thr Thr Asp	
65 70 75 80	
ctg ttt acg tat gtc cag gtg ccg gtt aac acc aat gct tcg atc atg	288
Leu Phe Thr Tyr Val Gln Val Pro Val Asn Thr Asn Ala Ser Ile Met	
85 90 95	
aag ggc att ata gtg ttg ttt atg cgg cgg cga ttt tca agg gct cag	336
Lys Gly Ile Ile Val Leu Phe Met Arg Arg Arg Phe Ser Arg Ala Gln	
100 105 110	
aag atg atg gac gcc atg gac att cga tgc acc aag atg gag gag aaa	384
Lys Met Met Asp Ala Met Asp Ile Arg Cys Thr Lys Met Glu Glu Lys	
115 120 125	
gtc cag gtg cac cga gca gca gcc tta tgc aat cgt gtt gtt gtg att	432
Val Gln Val His Arg Ala Ala Ala Leu Cys Asn Arg Val Val Val Ile	
130 135 140	
tac cat tgc ata tac ttc ggc tat cta tcc atg gcc tta acc gga gct	480
Tyr His Cys Ile Tyr Phe Gly Tyr Leu Ser Met Ala Leu Thr Gly Ala	
145 150 155 160	
ctg gtg att ggg aag act cca ttc tgt ttg tac aat cca ctg gtt aac	528
Leu Val Ile Gly Lys Thr Pro Phe Cys Leu Tyr Asn Pro Leu Val Asn	
165 170 175	
ccc gac gat cat ttc tat ctg gcc act gcc att gaa tcg gtc acc atg	576
Pro Asp Asp His Phe Tyr Leu Ala Thr Ala Ile Glu Ser Val Thr Met	
180 185 190	
gct ggc att att ctg gcc aat ctc att ttg gac gta tat ccc atc ata	624
Ala Gly Ile Ile Leu Ala Asn Leu Ile Leu Asp Val Tyr Pro Ile Ile	
195 200 205	
tat gtg gtc gtt ctg cgg atc cac atg gag ctc ttg agt gag cga atc	672
Tyr Val Val Val Leu Arg Ile His Met Glu Leu Leu Ser Glu Arg Ile	
210 215 220	
aag acg ctg cgt act gat gtg gaa aaa ggc gac gat caa cat tat gcc	720
Lys Thr Leu Arg Thr Asp Val Glu Lys Gly Asp Asp Gln His Tyr Ala	
225 230 235 240	
gag ctg gtg gag tgt gta aag gat cac aag cta att gtc gaa tat gga	768
Glu Leu Val Glu Cys Val Lys Asp His Lys Leu Ile Val Glu Tyr Gly	
245 250 255	

aac act ctg cgt ccc atg ata tcc gcc acg atg ttc atc caa cta cta 816
 Asn Thr Leu Arg Pro Met Ile Ser Ala Thr Met Phe Ile Gln Leu Leu
 260 265 270

tcc gtt ggc tta ctt ttg ggt ctg gca gcg gtg tcc atg cag ttc tat 864
 Ser Val Gly Leu Leu Leu Gly Leu Ala Ala Val Ser Met Gln Phe Tyr
 275 280 285

aac acc gta atg gag cgt gtt gtc tcc ggg gtc tac acc ata gcc att 912
 Asn Thr Val Met Glu Arg Val Val Ser Gly Val Tyr Thr Ile Ala Ile
 290 295 300

cta tcc cag acc ttt cca ttt tgc tat gtc tgt gag cag ctg agc agc 960
 Leu Ser Gln Thr Phe Pro Phe Cys Tyr Val Cys Glu Gln Leu Ser Ser
 305 310 315 320

gat tgc gaa tcc ctg acc aac aca ctg ttc cat tcc aag tgg att gga 1008
 Asp Cys Glu Ser Leu Thr Asn Thr Leu Phe His Ser Lys Trp Ile Gly
 325 330 335

gct gag cga cga tac aga acc acg atg ttg tac ttc att cac aat gtt 1056
 Ala Glu Arg Arg Tyr Arg Thr Thr Met Leu Tyr Phe Ile His Asn Val
 340 345 350

cag cag tcg att ttg ttc act gcg ggc gga att ttc ccc ata tgt cta 1104
 Gln Gln Ser Ile Leu Phe Thr Ala Gly Gly Ile Phe Pro Ile Cys Leu
 355 360 365

aac acc aat ata aag atg gcc aag ttc gct ttc tca gtg gtg acc att 1152
 Asn Thr Asn Ile Lys Met Ala Lys Phe Ala Phe Ser Val Val Thr Ile
 370 375 380

gta aat gag atg gac ttg gcc gag aaa ttg aga agg gag 1191
 Val Asn Glu Met Asp Leu Ala Glu Lys Leu Arg Arg Glu
 385 390 395

<210> 68
 <211> 397
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 68
 Met Ile Phe Lys Tyr Ile Gln Glu Pro Val Leu Gly Ser Leu Phe Arg
 1 5 10 15

Ser Arg Asp Ser Leu Ile Tyr Leu Asn Arg Ser Ile Asp Gln Met Gly

20	25	30
Trp Arg Leu Pro Pro Arg Thr Lys Pro Tyr Trp Trp Leu Tyr Tyr Ile		
35	40	45
Trp Thr Leu Val Val Ile Val Leu Val Phe Ile Phe Ile Pro Tyr Gly		
50	55	60
Leu Ile Met Thr Gly Ile Lys Glu Phe Lys Asn Phe Thr Thr Thr Asp		
65	70	75 80
Leu Phe Thr Tyr Val Gln Val Pro Val Asn Thr Asn Ala Ser Ile Met		
85	90	95
Lys Gly Ile Ile Val Leu Phe Met Arg Arg Arg Phe Ser Arg Ala Gln		
100	105	110
Lys Met Met Asp Ala Met Asp Ile Arg Cys Thr Lys Met Glu Glu Lys		
115	120	125
Val Gln Val His Arg Ala Ala Ala Leu Cys Asn Arg Val Val Val Ile		
130	135	140
Tyr His Cys Ile Tyr Phe Gly Tyr Leu Ser Met Ala Leu Thr Gly Ala		
145	150	155 160
Leu Val Ile Gly Lys Thr Pro Phe Cys Leu Tyr Asn Pro Leu Val Asn		
165	170	175
Pro Asp Asp His Phe Tyr Leu Ala Thr Ala Ile Glu Ser Val Thr Met		
180	185	190
Ala Gly Ile Ile Leu Ala Asn Leu Ile Leu Asp Val Tyr Pro Ile Ile		
195	200	205
Tyr Val Val Val Leu Arg Ile His Met Glu Leu Leu Ser Glu Arg Ile		
210	215	220
Lys Thr Leu Arg Thr Asp Val Glu Lys Gly Asp Asp Gln His Tyr Ala		
225	230	235 240
Glu Leu Val Glu Cys Val Lys Asp His Lys Leu Ile Val Glu Tyr Gly		
245	250	255
Asn Thr Leu Arg Pro Met Ile Ser Ala Thr Met Phe Ile Gln Leu Leu		
260	265	270
Ser Val Gly Leu Leu Leu Gly Leu Ala Ala Val Ser Met Gln Phe Tyr		

275		280		285
Asn Thr Val Met Glu Arg Val Val Ser Gly Val Tyr Thr Ile Ala Ile				
290		295		300
Leu Ser Gln Thr Phe Pro Phe Cys Tyr Val Cys Glu Gln Leu Ser Ser				
305		310		315
				320
Asp Cys Glu Ser Leu Thr Asn Thr Leu Phe His Ser Lys Trp Ile Gly				
	325		330	335
Ala Glu Arg Arg Tyr Arg Thr Thr Met Leu Tyr Phe Ile His Asn Val				
	340		345	350
Gln Gln Ser Ile Leu Phe Thr Ala Gly Gly Ile Phe Pro Ile Cys Leu				
	355		360	365
Asn Thr Asn Ile Lys Met Ala Lys Phe Ala Phe Ser Val Val Thr Ile				
	370		375	380
Val Asn Glu Met Asp Leu Ala Glu Lys Leu Arg Arg Glu				
	385		390	395

<210> 69
 <211> 1191
 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <222> (1)..(1191)
 <223> DORLU 5.1

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Met Leu Phe Asn Tyr Leu Arg Lys Pro Asn Pro Thr Asn Leu Leu Thr	
1 5 10 15	
tct ccg gac tca ttt aga tac ttt gag tat gga atg ttt tgc atg gga	96
Ser Pro Asp Ser Phe Arg Tyr Phe Glu Tyr Gly Met Phe Cys Met Gly	
20 25 30	
tgg cac aca cca gca acg cat aag ata atc tac tat ata aca tcc tgt	144
Trp His Thr Pro Ala Thr His Lys Ile Ile Tyr Tyr Ile Thr Ser Cys	
35 40 45	

ttg att ttt gct tgg tgt gcc gta tac ttg cca atc gga atc atc att	192
Leu Ile Phe Ala Trp Cys Ala Val Tyr Leu Pro Ile Gly Ile Ile Ile	
50 55 60	
agt ttc aaa acg gat att aac aca ttc aca ccg aat gaa ctg ttg aca	240
Ser Phe Lys Thr Asp Ile Asn Thr Phe Thr Pro Asn Glu Leu Leu Thr	
65 70 75 80	
gtt atg caa tta ttt ttc aat tca gtg gga atg cca ttc aag gtt ctg	288
Val Met Gln Leu Phe Phe Asn Ser Val Gly Met Pro Phe Lys Val Leu	
85 90 95	
ttc ttc aat ttg tat att tct gga ttt tac aag gcc aaa aag ctc ctt	336
Phe Phe Asn Leu Tyr Ile Ser Gly Phe Tyr Lys Ala Lys Lys Leu Leu	
100 105 110	
agc gaa atg gac aaa cgt tgc acc act ttg aag gag cga gtg gaa gtg	384
Ser Glu Met Asp Lys Arg Cys Thr Thr Leu Lys Glu Arg Val Glu Val	
115 120 125	
cac caa ggt gtg gtc cgt tgc aac aag gcc tac ctc att tac cag ttc	432
His Gln Gly Val Val Arg Cys Asn Lys Ala Tyr Leu Ile Tyr Gln Phe	
130 135 140	
att tat acc gcg tac act att tca aca ttt cta tcg gcg gct ctt agt	480
Ile Tyr Thr Ala Tyr Thr Ile Ser Thr Phe Leu Ser Ala Ala Leu Ser	
145 150 155 160	
gga aaa ttg cca tgg cgc atc tat aat cct ttt gtg gat ttt cga gaa	528
Gly Lys Leu Pro Trp Arg Ile Tyr Asn Pro Phe Val Asp Phe Arg Glu	
165 170 175	
agt aga tcc agt ttt tgg aaa gct gcc ctc aac gag aca gca ctt atg	576
Ser Arg Ser Ser Phe Trp Lys Ala Ala Leu Asn Glu Thr Ala Leu Met	
180 185 190	
cta ttt gct gtg act caa acc cta atg agt gat ata tat cca ctg ctt	624
Leu Phe Ala Val Thr Gln Thr Leu Met Ser Asp Ile Tyr Pro Leu Leu	
195 200 205	
tat ggt ttg atc ctg aga gtt cac ctc aaa ctt ttg cga cta aga gtg	672
Tyr Gly Leu Ile Leu Arg Val His Leu Lys Leu Leu Arg Leu Arg Val	
210 215 220	
gag agc ctg tgc aca gat tct gga aaa agc gat gct gaa aac gag caa	720
Glu Ser Leu Cys Thr Asp Ser Gly Lys Ser Asp Ala Glu Asn Glu Gln	
225 230 235 240	

gat ttg att aag tgc atc aag gat cac aat ctc att att gac tat gct	768
Asp Leu Ile Lys Cys Ile Lys Asp His Asn Leu Ile Ile Asp Tyr Ala	
245 250 255	
gca gca ata cga cca gcg gtt acc cgc aca att ttc gtt caa ttc ctc	816
Ala Ala Ile Arg Pro Ala Val Thr Arg Thr Ile Phe Val Gln Phe Leu	
260 265 270	
ttg atc gga att tgc ctt ggc ctt tca atg atc aat cta ctc ttc ttt	864
Leu Ile Gly Ile Cys Leu Gly Leu Ser Met Ile Asn Leu Leu Phe Phe	
275 280 285	
gcc gac atc tgg aca gga ttg gcc aca gtg gct tac atc aat ggt cta	912
Ala Asp Ile Trp Thr Gly Leu Ala Thr Val Ala Tyr Ile Asn Gly Leu	
290 295 300	
atg gtg cag aca ttt cca ttt tgc ttc gtt tgt gat cta ctc aaa aag	960
Met Val Gln Thr Phe Pro Phe Cys Phe Val Cys Asp Leu Leu Lys Lys	
305 310 315 320	
gat tgt gaa ctt ctt gtg tcg gcc ata ttt cat tcc aac tgg att aat	1008
Asp Cys Glu Leu Leu Val Ser Ala Ile Phe His Ser Asn Trp Ile Asn	
325 330 335	
tca agc cgc agt tac aag tca tct ttg aga tat ttt ctg aag aac gcc	1056
Ser Ser Arg Ser Tyr Lys Ser Ser Leu Arg Tyr Phe Leu Lys Asn Ala	
340 345 350	
cag aaa tca att gct ttt aca gcc ggc tct att ttt ccc att tct act	1104
Gln Lys Ser Ile Ala Phe Thr Ala Gly Ser Ile Phe Pro Ile Ser Thr	
355 360 365	
ggc tcg aat att aag gtg gct aag ctg gca ttt tcg gtg gtt act ttt	1152
Gly Ser Asn Ile Lys Val Ala Lys Leu Ala Phe Ser Val Val Thr Phe	
370 375 380	
gtc aat caa ctt aac ata gct gac aga ttg aca aag aac	1191
Val Asn Gln Leu Asn Ile Ala Asp Arg Leu Thr Lys Asn	
385 390 395	

<210> 70

<211> 397

<212> PRT

<213> Drosophila melanogaster

<400> 70

Met Leu Phe Asn Tyr Leu Arg Lys Pro Asn Pro Thr Asn Leu Leu Thr

1	5	10	15
Ser Pro Asp Ser Phe Arg Tyr Phe Glu Tyr Gly Met Phe Cys Met Gly	20	25	30
Trp His Thr Pro Ala Thr His Lys Ile Ile Tyr Tyr Ile Thr Ser Cys	35	40	45
Leu Ile Phe Ala Trp Cys Ala Val Tyr Leu Pro Ile Gly Ile Ile Ile	50	55	60
Ser Phe Lys Thr Asp Ile Asn Thr Phe Thr Pro Asn Glu Leu Leu Thr	65	70	75
Val Met Gln Leu Phe Phe Asn Ser Val Gly Met Pro Phe Lys Val Leu	85	90	95
Phe Phe Asn Leu Tyr Ile Ser Gly Phe Tyr Lys Ala Lys Lys Leu Leu	100	105	110
Ser Glu Met Asp Lys Arg Cys Thr Thr Leu Lys Glu Arg Val Glu Val	115	120	125
His Gln Gly Val Val Arg Cys Asn Lys Ala Tyr Leu Ile Tyr Gln Phe	130	135	140
Ile Tyr Thr Ala Tyr Thr Ile Ser Thr Phe Leu Ser Ala Ala Leu Ser	145	150	155
Gly Lys Leu Pro Trp Arg Ile Tyr Asn Pro Phe Val Asp Phe Arg Glu	165	170	175
Ser Arg Ser Ser Phe Trp Lys Ala Ala Leu Asn Glu Thr Ala Leu Met	180	185	190
Leu Phe Ala Val Thr Gln Thr Leu Met Ser Asp Ile Tyr Pro Leu Leu	195	200	205
Tyr Gly Leu Ile Leu Arg Val His Leu Lys Leu Leu Arg Leu Arg Val	210	215	220
Glu Ser Leu Cys Thr Asp Ser Gly Lys Ser Asp Ala Glu Asn Glu Gln	225	230	235
Asp Leu Ile Lys Cys Ile Lys Asp His Asn Leu Ile Ile Asp Tyr Ala	245	250	255
Ala Ala Ile Arg Pro Ala Val Thr Arg Thr Ile Phe Val Gln Phe Leu			

260	265	270
Leu Ile Gly Ile Cys Leu Gly Leu Ser Met Ile Asn Leu Leu Phe Phe		
275	280	285
Ala Asp Ile Trp Thr Gly Leu Ala Thr Val Ala Tyr Ile Asn Gly Leu		
290	295	300
Met Val Gln Thr Phe Pro Phe Cys Phe Val Cys Asp Leu Leu Lys Lys		
305	310	315
Asp Cys Glu Leu Leu Val Ser Ala Ile Phe His Ser Asn Trp Ile Asn		
325	330	335
Ser Ser Arg Ser Tyr Lys Ser Ser Leu Arg Tyr Phe Leu Lys Asn Ala		
340	345	350
Gln Lys Ser Ile Ala Phe Thr Ala Gly Ser Ile Phe Pro Ile Ser Thr		
355	360	365
Gly Ser Asn Ile Lys Val Ala Lys Leu Ala Phe Ser Val Val Thr Phe		
370	375	380
Val Asn Gln Leu Asn Ile Ala Asp Arg Leu Thr Lys Asn		
385	390	395

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 <211> 1239
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 <213> *Drosophila melanogaster*

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 <223> DORLU 6.1

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 Met Ala Val Ser Thr Arg Val Ala Thr Lys Gln Glu Val Pro Glu Ser
 1 5 10 15
 cgg cga gcg ttt agg aat ctc ttc aat tgc ttc tat gcc ctt ggc atg 96
 Arg Arg Ala Phe Arg Asn Leu Phe Asn Cys Phe Tyr Ala Leu Gly Met
 20 25 30
 cag gca ccg gat ggc agt cga ccg acc acg agc agc aca tgg caa cgc 144

Gln	Ala	Pro	Asp	Gly	Ser	Arg	Pro	Thr	Thr	Ser	Ser	Thr	Trp	Gln	Arg		
		35					40					45					
atc	tac	gcc	tgc	ttc	tcg	gtg	gtc	atg	tac	gtg	tgg	caa	ctg	ctg	ctg	192	
Ile	Tyr	Ala	Cys	Phe	Ser	Val	Val	Met	Tyr	Val	Trp	Gln	Leu	Leu	Leu		
	50					55					60						
gtg	ccc	aca	ttc	ttt	gtg	atc	agc	tat	cgg	tac	atg	ggc	ggc	atg	gag	240	
Val	Pro	Thr	Phe	Phe	Val	Ile	Ser	Tyr	Arg	Tyr	Met	Gly	Gly	Met	Glu		
	65				70				75						80		
att	acc	cag	gtg	ctg	acc	tcc	gcc	cag	gtg	gcc	atc	gat	gcg	gtc	att	288	
Ile	Thr	Gln	Val	Leu	Thr	Ser	Ala	Gln	Val	Ala	Ile	Asp	Ala	Val	Ile		
			85						90					95			
ctg	ccg	gcc	aag	att	gtg	gca	ctg	gcg	tgg	aat	ttg	cca	ttg	ctg	cgc	336	
Leu	Pro	Ala	Lys	Ile	Val	Ala	Leu	Ala	Trp	Asn	Leu	Pro	Leu	Leu	Arg		
			100					105						110			
aga	gca	gag	cat	cat	ctg	gcc	gcc	ttg	gat	gcg	cgg	tgc	agg	gaa	cag	384	
Arg	Ala	Glu	His	His	Leu	Ala	Ala	Leu	Asp	Ala	Arg	Cys	Arg	Glu	Gln		
		115					120					125					
gag	gag	ttc	caa	ttg	atc	ctc	gat	gcg	gtg	agg	ttt	tgc	aac	tat	ctg	432	
Glu	Glu	Phe	Gln	Leu	Ile	Leu	Asp	Ala	Val	Arg	Phe	Cys	Asn	Tyr	Leu		
	130					135					140						
gta	tgg	ttc	tac	cag	atc	tgc	tat	gcc	atc	tac	tcc	tcg	tcg	aca	ttt	480	
Val	Trp	Phe	Tyr	Gln	Ile	Cys	Tyr	Ala	Ile	Tyr	Ser	Ser	Ser	Thr	Phe		
	145				150					155					160		
gtg	tgc	gcc	ttc	ctg	ctg	ggc	caa	ccg	cca	tat	gcc	ctc	tat	ttg	cct	528	
Val	Cys	Ala	Phe	Leu	Leu	Gly	Gln	Pro	Pro	Tyr	Ala	Leu	Tyr	Leu	Pro		
				165					170					175			
ggc	ctc	gat	tgg	cag	cgt	tcc	cag	atg	cag	ttc	tgc	atc	cag	gcc	tgg	576	
Gly	Leu	Asp	Trp	Gln	Arg	Ser	Gln	Met	Gln	Phe	Cys	Ile	Gln	Ala	Trp		
			180					185					190				
att	gag	ttc	ctt	atc	atg	aac	tgg	acg	tgc	ctg	cac	caa	gct	agc	gat	624	
Ile	Glu	Phe	Leu	Ile	Met	Asn	Trp	Thr	Cys	Leu	His	Gln	Ala	Ser	Asp		
		195					200					205					
gat	gtg	tac	gcc	gtt	atc	tat	ctg	tat	gtg	gtc	cgg	att	caa	gtg	caa	672	
Asp	Val	Tyr	Ala	Val	Ile	Tyr	Leu	Tyr	Val	Val	Arg	Ile	Gln	Val	Gln		
	210					215					220						
ttg	ctg	gcc	agg	cgg	gtg	gag	aag	ctg	ggc	acg	gat	gat	agt	ggc	cag	720	

Leu	Leu	Ala	Arg	Arg	Val	Glu	Lys	Leu	Gly	Thr	Asp	Asp	Ser	Gly	Gln		
225					230					235					240		
gtg	gag	atc	tat	ccc	gat	gag	cgg	cgg	cag	gag	gag	cat	tgc	gcg	gaa	768	
Val	Glu	Ile	Tyr	Pro	Asp	Glu	Arg	Arg	Gln	Glu	Glu	His	Cys	Ala	Glu		
				245					250					255			
ctg	cag	cgc	tgc	att	gta	gat	cac	cag	acg	atg	ctg	cag	ctg	ctc	gac	816	
Leu	Gln	Arg	Cys	Ile	Val	Asp	His	Gln	Thr	Met	Leu	Gln	Leu	Leu	Asp		
				260				265					270				
tgc	att	agt	ccc	gtc	atc	tcg	cgt	acc	ata	ttc	gtt	cag	ttc	ctg	atc	864	
Cys	Ile	Ser	Pro	Val	Ile	Ser	Arg	Thr	Ile	Phe	Val	Gln	Phe	Leu	Ile		
		275					280					285					
acc	gcc	gcc	atc	atg	ggc	acc	acc	atg	atc	aac	att	ttc	att	ttc	gcc	912	
Thr	Ala	Ala	Ile	Met	Gly	Thr	Thr	Met	Ile	Asn	Ile	Phe	Ile	Phe	Ala		
		290				295				300							
aat	acg	aac	acg	aag	atc	gca	tcg	atc	att	tac	ctg	ctg	gcg	gtg	acc	960	
Asn	Thr	Asn	Thr	Lys	Ile	Ala	Ser	Ile	Ile	Tyr	Leu	Leu	Ala	Val	Thr		
305					310					315					320		
ctg	cag	acg	gct	cca	tgt	tgc	tat	cag	gcc	acc	tcg	ctg	atg	ttg	gac	1008	
Leu	Gln	Thr	Ala	Pro	Cys	Cys	Tyr	Gln	Ala	Thr	Ser	Leu	Met	Leu	Asp		
				325				330						335			
aac	gag	agg	ctg	gcc	ctg	gcc	atc	ttc	cag	tgc	cag	tgg	ctg	ggc	cag	1056	
Asn	Glu	Arg	Leu	Ala	Leu	Ala	Ile	Phe	Gln	Cys	Gln	Trp	Leu	Gly	Gln		
			340					345					350				
agt	gcc	cgg	ttc	cgt	aag	atg	ctg	ctc	tac	tat	ctt	cat	cgc	gcc	cag	1104	
Ser	Ala	Arg	Phe	Arg	Lys	Met	Leu	Leu	Tyr	Tyr	Leu	His	Arg	Ala	Gln		
		355					360					365					
cag	ccc	atc	acg	ctg	acc	gcc	atg	aag	ctg	ttt	ccc	atc	aat	ctg	gcc	1152	
Gln	Pro	Ile	Thr	Leu	Thr	Ala	Met	Lys	Leu	Phe	Pro	Ile	Asn	Leu	Ala		
		370				375					380						
acg	tac	ttc	agt	ata	gcc	aag	ttc	tcg	ttt	tcg	ctc	tac	acg	ctc	atc	1200	
Thr	Tyr	Phe	Ser	Ile	Ala	Lys	Phe	Ser	Phe	Ser	Leu	Tyr	Thr	Leu	Ile		
385					390				395					400			
aag	ggg	atg	aat	ctc	ggc	gag	cga	ttc	aac	agg	aca	aat				1239	
Lys	Gly	Met	Asn	Leu	Gly	Glu	Arg	Phe	Asn	Arg	Thr	Asn					
				405					410								

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<211> 413

<212> PRT

<213> *Drosophila melanogaster*

<400> 72

Met Ala Val Ser Thr Arg Val Ala Thr Lys Gln Glu Val Pro Glu Ser
1 5 10 15

Arg Arg Ala Phe Arg Asn Leu Phe Asn Cys Phe Tyr Ala Leu Gly Met
20 25 30

Gln Ala Pro Asp Gly Ser Arg Pro Thr Thr Ser Ser Thr Trp Gln Arg
35 40 45

Ile Tyr Ala Cys Phe Ser Val Val Met Tyr Val Trp Gln Leu Leu Leu
50 55 60

Val Pro Thr Phe Phe Val Ile Ser Tyr Arg Tyr Met Gly Gly Met Glu
65 70 75 80

Ile Thr Gln Val Leu Thr Ser Ala Gln Val Ala Ile Asp Ala Val Ile
85 90 95

Leu Pro Ala Lys Ile Val Ala Leu Ala Trp Asn Leu Pro Leu Leu Arg
100 105 110

Arg Ala Glu His His Leu Ala Ala Leu Asp Ala Arg Cys Arg Glu Gln
115 120 125

Glu Glu Phe Gln Leu Ile Leu Asp Ala Val Arg Phe Cys Asn Tyr Leu
130 135 140

Val Trp Phe Tyr Gln Ile Cys Tyr Ala Ile Tyr Ser Ser Ser Thr Phe
145 150 155 160

Val Cys Ala Phe Leu Leu Gly Gln Pro Pro Tyr Ala Leu Tyr Leu Pro
165 170 175

Gly Leu Asp Trp Gln Arg Ser Gln Met Gln Phe Cys Ile Gln Ala Trp
180 185 190

Ile Glu Phe Leu Ile Met Asn Trp Thr Cys Leu His Gln Ala Ser Asp
195 200 205

Asp Val Tyr Ala Val Ile Tyr Leu Tyr Val Val Arg Ile Gln Val Gln
210 215 220

Leu Leu Ala Arg Arg Val Glu Lys Leu Gly Thr Asp Asp Ser Gly Gln
 225 230 235 240
 Val Glu Ile Tyr Pro Asp Glu Arg Arg Gln Glu Glu His Cys Ala Glu
 245 250 255
 Leu Gln Arg Cys Ile Val Asp His Gln Thr Met Leu Gln Leu Leu Asp
 260 265 270
 Cys Ile Ser Pro Val Ile Ser Arg Thr Ile Phe Val Gln Phe Leu Ile
 275 280 285
 Thr Ala Ala Ile Met Gly Thr Thr Met Ile Asn Ile Phe Ile Phe Ala
 290 295 300
 Asn Thr Asn Thr Lys Ile Ala Ser Ile Ile Tyr Leu Leu Ala Val Thr
 305 310 315 320
 Leu Gln Thr Ala Pro Cys Cys Tyr Gln Ala Thr Ser Leu Met Leu Asp
 325 330 335
 Asn Glu Arg Leu Ala Leu Ala Ile Phe Gln Cys Gln Trp Leu Gly Gln
 340 345 350
 Ser Ala Arg Phe Arg Lys Met Leu Leu Tyr Tyr Leu His Arg Ala Gln
 355 360 365
 Gln Pro Ile Thr Leu Thr Ala Met Lys Leu Phe Pro Ile Asn Leu Ala
 370 375 380
 Thr Tyr Phe Ser Ile Ala Lys Phe Ser Phe Ser Leu Tyr Thr Leu Ile
 385 390 395 400
 Lys Gly Met Asn Leu Gly Glu Arg Phe Asn Arg Thr Asn
 405 410

<210> 73
 <211> 1089
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
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 <222> (1)..(1089)
 <223> DORLU 7.1

<400> 73

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Met	Asp	Tyr	Asp	Arg	Ile	Arg	Pro	Val	Arg	Phe	Leu	Thr	Gly	Val	Leu	
1				5				10						15		

aaa	tgg	tgg	cgt	ctc	tgg	ccg	agg	aag	gaa	tcg	gtg	tcc	aca	ccg	gac	96
Lys	Trp	Trp	Arg	Leu	Trp	Pro	Arg	Lys	Glu	Ser	Val	Ser	Thr	Pro	Asp	
			20					25					30			

tgg	act	aac	tgg	cag	gca	tat	gcc	ttg	cac	gtt	cca	ttt	aca	ttc	ttg	144
Trp	Thr	Asn	Trp	Gln	Ala	Tyr	Ala	Leu	His	Val	Pro	Phe	Thr	Phe	Leu	
		35					40					45				

ttt	gtg	ttg	ctt	ttg	tgg	ttg	gag	gca	atc	aag	agc	agg	gat	ata	cag	192
Phe	Val	Leu	Leu	Leu	Trp	Leu	Glu	Ala	Ile	Lys	Ser	Arg	Asp	Ile	Gln	
	50					55					60					

cat	acc	gcc	gat	gtc	ctt	ttg	att	tgc	cta	acc	acc	act	gcc	ttg	gga	240
His	Thr	Ala	Asp	Val	Leu	Leu	Ile	Cys	Leu	Thr	Thr	Thr	Ala	Leu	Gly	
	65				70					75					80	

ggt	aaa	gtt	atc	aat	atc	tgg	aag	tat	gcc	cat	gtg	gcc	caa	ggc	att	288
Gly	Lys	Val	Ile	Asn	Ile	Trp	Lys	Tyr	Ala	His	Val	Ala	Gln	Gly	Ile	
				85				90					95			

ttg	tcc	gag	tgg	agc	acg	tgg	gat	ctt	ttc	gag	ctg	agg	agc	aaa	cag	336
Leu	Ser	Glu	Trp	Ser	Thr	Trp	Asp	Leu	Phe	Glu	Leu	Arg	Ser	Lys	Gln	
		100					105						110			

gaa	gtg	gat	atg	tgg	cga	ttc	gag	cat	cga	cgt	ttc	aat	cgt	gtt	ttt	384
Glu	Val	Asp	Met	Trp	Arg	Phe	Glu	His	Arg	Arg	Phe	Asn	Arg	Val	Phe	
	115					120						125				

atg	ttt	tac	tgt	ttg	tgc	agt	gct	ggt	gta	atc	cca	ttt	att	gtg	att	432
Met	Phe	Tyr	Cys	Leu	Cys	Ser	Ala	Gly	Val	Ile	Pro	Phe	Ile	Val	Ile	
	130					135					140					

caa	ccg	ttg	ttt	gat	atc	cca	aat	cga	ttg	ccc	ttc	tgg	atg	tgg	aca	480
Gln	Pro	Leu	Phe	Asp	Ile	Pro	Asn	Arg	Leu	Pro	Phe	Trp	Met	Trp	Thr	
145					150					155					160	

cca	ttc	gat	tgg	cag	cag	cct	gtt	ctc	tta	tgg	tat	gca	ttc	atc	tat	528
Pro	Phe	Asp	Trp	Gln	Gln	Pro	Val	Leu	Leu	Trp	Tyr	Ala	Phe	Ile	Tyr	
				165				170					175			

cag	gcc	aca	acc	att	cct	att	gcc	tgt	gct	tgc	aac	gta	acc	atg	gac	576
Gln	Ala	Thr	Thr	Ile	Pro	Ile	Ala	Cys	Ala	Cys	Asn	Val	Thr	Met	Asp	
		180					185					190				

gct gtt aat tgg tac ttg atg ctg cat ctg tcc ttg tgt ttg cgt atg	624
Ala Val Asn Trp Tyr Leu Met Leu His Leu Ser Leu Cys Leu Arg Met	
195 200 205	
ttg ggc cag cga ttg agt aag ctt cag cat gat gac aag gat ctg agg	672
Leu Gly Gln Arg Leu Ser Lys Leu Gln His Asp Asp Lys Asp Leu Arg	
210 215 220	
gag aag ttc ctg gaa ctg atc cat ctg cac cag cga ctc aag caa cag	720
Glu Lys Phe Leu Glu Leu Ile His Leu His Gln Arg Leu Lys Gln Gln	
225 230 235 240	
gcc ttg agc att gaa atc ttt att tcg aag agc acg ttc acc caa att	768
Ala Leu Ser Ile Glu Ile Phe Ile Ser Lys Ser Thr Phe Thr Gln Ile	
245 250 255	
ctg gtc agt tcc ctt atc att tgc ttc acc att tac agc atg cag atg	816
Leu Val Ser Ser Leu Ile Ile Cys Phe Thr Ile Tyr Ser Met Gln Met	
260 265 270	
tac cta gtg gcc atg atc atg cag gtc atg ctg ccc acc ata tat ggt	864
Tyr Leu Val Ala Met Ile Met Gln Val Met Leu Pro Thr Ile Tyr Gly	
275 280 285	
aac gcc gtc atc gat tct gca aat atg ttg acc gat tcc atg tac aat	912
Asn Ala Val Ile Asp Ser Ala Asn Met Leu Thr Asp Ser Met Tyr Asn	
290 295 300	
tcg gat tgg ccg gat atg aat tgc cga atg cgt cgc cta gtt tta atg	960
Ser Asp Trp Pro Asp Met Asn Cys Arg Met Arg Arg Leu Val Leu Met	
305 310 315 320	
ttt atg gtg tac tta aat cga ccg gtg acc tta aaa gcc ggt ggc ttt	1008
Phe Met Val Tyr Leu Asn Arg Pro Val Thr Leu Lys Ala Gly Gly Phe	
325 330 335	
ttt cat att ggt tta cct ctg ttt acc aag acc atg aat caa gca tac	1056
Phe His Ile Gly Leu Pro Leu Phe Thr Lys Thr Met Asn Gln Ala Tyr	
340 345 350	
agt ttg ctg gcc ttg ctg ctc aac atg aac caa	1089
Ser Leu Leu Ala Leu Leu Leu Asn Met Asn Gln	
355 360	

<210> 74

<211> 363

<212> PRT

<213> *Drosophila melanogaster*

<400> 74

Met Asp Tyr Asp Arg Ile Arg Pro Val Arg Phe Leu Thr Gly Val Leu
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Lys Trp Trp Arg Leu Trp Pro Arg Lys Glu Ser Val Ser Thr Pro Asp
20 25 30

Trp Thr Asn Trp Gln Ala Tyr Ala Leu His Val Pro Phe Thr Phe Leu
35 40 45

Phe Val Leu Leu Leu Trp Leu Glu Ala Ile Lys Ser Arg Asp Ile Gln
50 55 60

His Thr Ala Asp Val Leu Leu Ile Cys Leu Thr Thr Thr Ala Leu Gly
65 70 75 80

Gly Lys Val Ile Asn Ile Trp Lys Tyr Ala His Val Ala Gln Gly Ile
85 90 95

Leu Ser Glu Trp Ser Thr Trp Asp Leu Phe Glu Leu Arg Ser Lys Gln
100 105 110

Glu Val Asp Met Trp Arg Phe Glu His Arg Arg Phe Asn Arg Val Phe
115 120 125

Met Phe Tyr Cys Leu Cys Ser Ala Gly Val Ile Pro Phe Ile Val Ile
130 135 140

Gln Pro Leu Phe Asp Ile Pro Asn Arg Leu Pro Phe Trp Met Trp Thr
145 150 155 160

Pro Phe Asp Trp Gln Gln Pro Val Leu Leu Trp Tyr Ala Phe Ile Tyr
165 170 175

Gln Ala Thr Thr Ile Pro Ile Ala Cys Ala Cys Asn Val Thr Met Asp
180 185 190

Ala Val Asn Trp Tyr Leu Met Leu His Leu Ser Leu Cys Leu Arg Met
195 200 205

Leu Gly Gln Arg Leu Ser Lys Leu Gln His Asp Asp Lys Asp Leu Arg
210 215 220

Glu Lys Phe Leu Glu Leu Ile His Leu His Gln Arg Leu Lys Gln Gln
225 230 235 240

Ala Leu Ser Ile Glu Ile Phe Ile Ser Lys Ser Thr Phe Thr Gln Ile
245 250 255

Leu Val Ser Ser Leu Ile Ile Cys Phe Thr Ile Tyr Ser Met Gln Met
260 265 270

Tyr Leu Val Ala Met Ile Met Gln Val Met Leu Pro Thr Ile Tyr Gly
275 280 285

Asn Ala Val Ile Asp Ser Ala Asn Met Leu Thr Asp Ser Met Tyr Asn
290 295 300

Ser Asp Trp Pro Asp Met Asn Cys Arg Met Arg Arg Leu Val Leu Met
305 310 315 320

Phe Met Val Tyr Leu Asn Arg Pro Val Thr Leu Lys Ala Gly Gly Phe
325 330 335

Phe His Ile Gly Leu Pro Leu Phe Thr Lys Thr Met Asn Gln Ala Tyr
340 345 350

Ser Leu Leu Ala Leu Leu Leu Asn Met Asn Gln
355 360

<210> 75

<211> 1176

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1176)

<223> DORLU 9.1

<400> 75

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Met Ser Asp Lys Val Lys Gly Lys Lys Gln Glu Glu Lys Asp Gln Ser
1 5 10 15

ttg cgg gtg caa att ctc gtt tat cgc tgc atg ggc atc gat ttg tgg 96
Leu Arg Val Gln Ile Leu Val Tyr Arg Cys Met Gly Ile Asp Leu Trp
20 25 30

agc ccc acg atg gcg aat gac cgc ccg tgg ctg acc ttt gtc aca atg 144
Ser Pro Thr Met Ala Asn Asp Arg Pro Trp Leu Thr Phe Val Thr Met

35	40	45	
gga cca ctt ttc ctg ttt atg gtg ccc atg ttc ctg gcc gcc cac gag			192
Gly Pro Leu Phe Leu Phe Met Val Pro Met Phe Leu Ala Ala His Glu			
50	55	60	
tac atc acc cag gtg agc ctg ctc tcc gac acc ctg ggc tcc acc ttc			240
Tyr Ile Thr Gln Val Ser Leu Leu Ser Asp Thr Leu Gly Ser Thr Phe			
65	70	75	80
gcc agc atg ctc acc ctg gtc aaa ttc ctg ctc ttc tgc tat cat cgc			288
Ala Ser Met Leu Thr Leu Val Lys Phe Leu Leu Phe Cys Tyr His Arg			
85	90	95	
aag gag ttc gtc ggc ctg atc tac cac atc agg gcc att ctg gct aaa			336
Lys Glu Phe Val Gly Leu Ile Tyr His Ile Arg Ala Ile Leu Ala Lys			
100	105	110	
gaa atc gaa gtg tgg cct gat gcg cgg gaa atc atc gag gtg gag aac			384
Glu Ile Glu Val Trp Pro Asp Ala Arg Glu Ile Ile Glu Val Glu Asn			
115	120	125	
caa agt gac caa atg ctc agt ctt acg tac act cgc tgt ttt gga ctg			432
Gln Ser Asp Gln Met Leu Ser Leu Thr Tyr Thr Arg Cys Phe Gly Leu			
130	135	140	
gct gga atc ttt gcg gcc ctg aag ccc ttt gtg ggc atc ata ctc tcc			480
Ala Gly Ile Phe Ala Ala Leu Lys Pro Phe Val Gly Ile Ile Leu Ser			
145	150	155	160
tcg att cgc ggc gac gag att cac ctg gag ctg ccc cac aac ggc gtt			528
Ser Ile Arg Gly Asp Glu Ile His Leu Glu Leu Pro His Asn Gly Val			
165	170	175	
tac ccg tac gat ctc cag gtg gtc atg ttt tat gtg ccc acc tat ctg			576
Tyr Pro Tyr Asp Leu Gln Val Val Met Phe Tyr Val Pro Thr Tyr Leu			
180	185	190	
tgg aat gtg atg gcc agc tat agt gct gta acc atg gca ctc tgc gtg			624
Trp Asn Val Met Ala Ser Tyr Ser Ala Val Thr Met Ala Leu Cys Val			
195	200	205	
gac tcg ctg ctc ttc ttt ttc acc tac aac gtg tgc gcc att ttc aag			672
Asp Ser Leu Leu Phe Phe Phe Thr Tyr Asn Val Cys Ala Ile Phe Lys			
210	215	220	
atc gcc aag cac cgg atg atc cat ctg ccg gcg gtg ggc gga aag gag			720
Ile Ala Lys His Arg Met Ile His Leu Pro Ala Val Gly Gly Lys Glu			

225	230	235	240	
gag ctg gag ggg ctc gtc cag gtg ctg ctg ctg cac cag aag ggc ctc				768
Glu Leu Glu Gly Leu Val Gln Val Leu Leu Leu His Gln Lys Gly Leu				
	245	250	255	
cag atc gcc gat cac att gcg gac aag tac cgg ccg ctg atc ttt ttg				816
Gln Ile Ala Asp His Ile Ala Asp Lys Tyr Arg Pro Leu Ile Phe Leu				
	260	265	270	
cag ttc ttt ctg tcc gcc ttg cag atc tgc ttc att gga ttc cag gtg				864
Gln Phe Phe Leu Ser Ala Leu Gln Ile Cys Phe Ile Gly Phe Gln Val				
	275	280	285	
gct gat ctg ttt ccc aat ccg cag agt ctc tac ttt atc gcc ttt gtg				912
Ala Asp Leu Phe Pro Asn Pro Gln Ser Leu Tyr Phe Ile Ala Phe Val				
	290	295	300	
ggc tcg ctg ctc atc gca ctg ttc atc tac tcg aag tgc ggc gaa aat				960
Gly Ser Leu Leu Ile Ala Leu Phe Ile Tyr Ser Lys Cys Gly Glu Asn				
	305	310	315	320
atc aag agt gcc agc ctg gat ttc gga aac ggg ctg tac gag acc aac				1008
Ile Lys Ser Ala Ser Leu Asp Phe Gly Asn Gly Leu Tyr Glu Thr Asn				
	325	330	335	
tgg acc gac ttc tcg cca ccc act aaa aga gcc ctc ctc att gcc gcc				1056
Trp Thr Asp Phe Ser Pro Pro Thr Lys Arg Ala Leu Leu Ile Ala Ala				
	340	345	350	
atg cgc gcc cag cga cct tgc cag atg aag ggc tac ttt ttc gag gcc				1104
Met Arg Ala Gln Arg Pro Cys Gln Met Lys Gly Tyr Phe Phe Glu Ala				
	355	360	365	
agc atg gcc acc ttc tcg acg att gtt cgc tct gcc gtg tcg tac atc				1152
Ser Met Ala Thr Phe Ser Thr Ile Val Arg Ser Ala Val Ser Tyr Ile				
	370	375	380	
atg atg ttg cgc tcc ttt aat gcc				1176
Met Met Leu Arg Ser Phe Asn Ala				
	385	390		

<210> 76

<211> 392

<212> PRT

<213> Drosophila melanogaster

<400> 76

Met	Ser	Asp	Lys	Val	Lys	Gly	Lys	Lys	Gln	Glu	Glu	Lys	Asp	Gln	Ser	
1				5					10					15		
Leu	Arg	Val	Gln	Ile	Leu	Val	Tyr	Arg	Cys	Met	Gly	Ile	Asp	Leu	Trp	
			20					25					30			
Ser	Pro	Thr	Met	Ala	Asn	Asp	Arg	Pro	Trp	Leu	Thr	Phe	Val	Thr	Met	
		35					40					45				
Gly	Pro	Leu	Phe	Leu	Phe	Met	Val	Pro	Met	Phe	Leu	Ala	Ala	His	Glu	
	50					55					60					
Tyr	Ile	Thr	Gln	Val	Ser	Leu	Leu	Ser	Asp	Thr	Leu	Gly	Ser	Thr	Phe	
65					70					75					80	
Ala	Ser	Met	Leu	Thr	Leu	Val	Lys	Phe	Leu	Leu	Phe	Cys	Tyr	His	Arg	
				85					90						95	
Lys	Glu	Phe	Val	Gly	Leu	Ile	Tyr	His	Ile	Arg	Ala	Ile	Leu	Ala	Lys	
			100					105					110			
Glu	Ile	Glu	Val	Trp	Pro	Asp	Ala	Arg	Glu	Ile	Ile	Glu	Val	Glu	Asn	
			115				120					125				
Gln	Ser	Asp	Gln	Met	Leu	Ser	Leu	Thr	Tyr	Thr	Arg	Cys	Phe	Gly	Leu	
			130				135				140					
Ala	Gly	Ile	Phe	Ala	Ala	Leu	Lys	Pro	Phe	Val	Gly	Ile	Ile	Leu	Ser	
145					150					155					160	
Ser	Ile	Arg	Gly	Asp	Glu	Ile	His	Leu	Glu	Leu	Pro	His	Asn	Gly	Val	
				165					170					175		
Tyr	Pro	Tyr	Asp	Leu	Gln	Val	Val	Met	Phe	Tyr	Val	Pro	Thr	Tyr	Leu	
			180					185						190		
Trp	Asn	Val	Met	Ala	Ser	Tyr	Ser	Ala	Val	Thr	Met	Ala	Leu	Cys	Val	
			195					200				205				
Asp	Ser	Leu	Leu	Phe	Phe	Phe	Thr	Tyr	Asn	Val	Cys	Ala	Ile	Phe	Lys	
		210				215					220					
Ile	Ala	Lys	His	Arg	Met	Ile	His	Leu	Pro	Ala	Val	Gly	Gly	Lys	Glu	
225					230					235					240	
Glu	Leu	Glu	Gly	Leu	Val	Gln	Val	Leu	Leu	Leu	His	Gln	Lys	Gly	Leu	
				245					250					255		

Gln Ile Ala Asp His Ile Ala Asp Lys Tyr Arg Pro Leu Ile Phe Leu
 260 265 270

Gln Phe Phe Leu Ser Ala Leu Gln Ile Cys Phe Ile Gly Phe Gln Val
 275 280 285

Ala Asp Leu Phe Pro Asn Pro Gln Ser Leu Tyr Phe Ile Ala Phe Val
 290 295 300

Gly Ser Leu Leu Ile Ala Leu Phe Ile Tyr Ser Lys Cys Gly Glu Asn
 305 310 315 320

Ile Lys Ser Ala Ser Leu Asp Phe Gly Asn Gly Leu Tyr Glu Thr Asn
 325 330 335

Trp Thr Asp Phe Ser Pro Pro Thr Lys Arg Ala Leu Leu Ile Ala Ala
 340 345 350

Met Arg Ala Gln Arg Pro Cys Gln Met Lys Gly Tyr Phe Phe Glu Ala
 355 360 365

Ser Met Ala Thr Phe Ser Thr Ile Val Arg Ser Ala Val Ser Tyr Ile
 370 375 380

Met Met Leu Arg Ser Phe Asn Ala
 385 390

<210> 77

<211> 1221

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1221)

<223> DORLU 12.1

<400> 77

atg gat aac gtc gcg gaa atg cct gaa gaa aag tat gtc gaa gtc gat 48
 Met Asp Asn Val Ala Glu Met Pro Glu Glu Lys Tyr Val Glu Val Asp
 1 5 10 15

gat ttt ttg agg cta gct gtg aaa ttc tac aat act ttg ggc att gat 96
 Asp Phe Leu Arg Leu Ala Val Lys Phe Tyr Asn Thr Leu Gly Ile Asp
 20 25 30

ccc tat gaa act gga cga aaa cga act att tgg ttt caa ata tat ttc	144
Pro Tyr Glu Thr Gly Arg Lys Arg Thr Ile Trp Phe Gln Ile Tyr Phe	
35 40 45	
gca ttg aat atg ttt aat atg gtg ttt agt ttt tat gcc gag gta gcg	192
Ala Leu Asn Met Phe Asn Met Val Phe Ser Phe Tyr Ala Glu Val Ala	
50 55 60	
act ctg gtg gac agg tta cgc gat aat gaa aat ttt ctc gag agc tgc	240
Thr Leu Val Asp Arg Leu Arg Asp Asn Glu Asn Phe Leu Glu Ser Cys	
65 70 75 80	
atc tta ctg agc tac gtg tcc ttt gtg gtc atg ggc ctc tcc aag ata	288
Ile Leu Leu Ser Tyr Val Ser Phe Val Val Met Gly Leu Ser Lys Ile	
85 90 95	
ggt gct gta atg aaa aaa aag cca aaa atg aca gct ttg gtc agg caa	336
Gly Ala Val Met Lys Lys Lys Pro Lys Met Thr Ala Leu Val Arg Gln	
100 105 110	
ttg gag acc tgc ttt ccg tcg cca agt gca aag gtt caa gag gaa tat	384
Leu Glu Thr Cys Phe Pro Ser Pro Ser Ala Lys Val Gln Glu Glu Tyr	
115 120 125	
gct gtg aag tcc tgg ctg aaa cgc tgc cat ata tac aca aag gga ttt	432
Ala Val Lys Ser Trp Leu Lys Arg Cys His Ile Tyr Thr Lys Gly Phe	
130 135 140	
ggt ggt ctc ttc atg atc atg tat ttc gct cac gct ctg att ccc tta	480
Gly Gly Leu Phe Met Ile Met Tyr Phe Ala His Ala Leu Ile Pro Leu	
145 150 155 160	
ttc ata tac ttc att caa aga gtg ctg ctc cac tat ccg gat gcc aag	528
Phe Ile Tyr Phe Ile Gln Arg Val Leu Leu His Tyr Pro Asp Ala Lys	
165 170 175	
cag att atg ccg ttt tac caa ctc gaa cct tgg gaa ttt cgc gac tcc	576
Gln Ile Met Pro Phe Tyr Gln Leu Glu Pro Trp Glu Phe Arg Asp Ser	
180 185 190	
tgg ttg ttt tat cca agc tat ttt cac cag tcg tcg gcc gga tat acg	624
Trp Leu Phe Tyr Pro Ser Tyr Phe His Gln Ser Ser Ala Gly Tyr Thr	
195 200 205	
gct aca tgt gga tcc att gcc ggt gac cta atg atc ttc gct gtg gtc	672
Ala Thr Cys Gly Ser Ile Ala Gly Asp Leu Met Ile Phe Ala Val Val	
210 215 220	

[illegible]

<210> 78
 <211> 407
 <212> PRT
 <213> Drosophila melanogaster

<400> 78

Met Asp Asn Val Ala Glu Met Pro Glu Glu Lys Tyr Val Glu Val Asp
 1 5 10 15

Asp Phe Leu Arg Leu Ala Val Lys Phe Tyr Asn Thr Leu Gly Ile Asp
 20 25 30

Pro Tyr Glu Thr Gly Arg Lys Arg Thr Ile Trp Phe Gln Ile Tyr Phe
 35 40 45

Ala Leu Asn Met Phe Asn Met Val Phe Ser Phe Tyr Ala Glu Val Ala
 50 55 60

Thr Leu Val Asp Arg Leu Arg Asp Asn Glu Asn Phe Leu Glu Ser Cys
 65 70 75 80

Ile Leu Leu Ser Tyr Val Ser Phe Val Val Met Gly Leu Ser Lys Ile
 85 90 95

Gly Ala Val Met Lys Lys Lys Pro Lys Met Thr Ala Leu Val Arg Gln
 100 105 110

Leu Glu Thr Cys Phe Pro Ser Pro Ser Ala Lys Val Gln Glu Glu Tyr
 115 120 125

Ala Val Lys Ser Trp Leu Lys Arg Cys His Ile Tyr Thr Lys Gly Phe
 130 135 140

Gly Gly Leu Phe Met Ile Met Tyr Phe Ala His Ala Leu Ile Pro Leu
 145 150 155 160

Phe Ile Tyr Phe Ile Gln Arg Val Leu Leu His Tyr Pro Asp Ala Lys
 165 170 175

Gln Ile Met Pro Phe Tyr Gln Leu Glu Pro Trp Glu Phe Arg Asp Ser
 180 185 190

Trp Leu Phe Tyr Pro Ser Tyr Phe His Gln Ser Ser Ala Gly Tyr Thr
 195 200 205

Ala Thr Cys Gly Ser Ile Ala Gly Asp Leu Met Ile Phe Ala Val Val

210	215	220
Leu Gln Val Ile Met His Tyr Glu Arg Leu Ala Lys Val Leu Arg Glu		
225	230	235 240
Phe Lys Ile Gln Ala His Asn Ala Pro Asn Gly Ala Lys Glu Asp Ile		
	245	250 255
Arg Lys Leu Gln Ser Leu Val Ala Asn His Ile Asp Ile Leu Arg Leu		
	260	265 270
Thr Asp Leu Met Asn Glu Val Phe Gly Ile Pro Leu Leu Leu Asn Phe		
	275	280 285
Ile Ala Ser Ala Leu Leu Val Cys Leu Val Gly Val Gln Leu Thr Ile		
	290	295 300
Ala Leu Ser Pro Glu Tyr Phe Cys Lys Gln Met Leu Phe Leu Ile Ser		
305	310	315 320
Val Leu Leu Glu Val Tyr Leu Leu Cys Ser Phe Ser Gln Arg Leu Ile		
	325	330 335
Asp Ala Ser Glu Asn Val Gly His Ala Ala Tyr Asp Met Asp Trp Leu		
	340	345 350
Gly Ser Asp Lys Arg Phe Lys Lys Ile Leu Ile Phe Ile Ser Met Arg		
	355	360 365
Ser Gln Lys Pro Val Cys Leu Lys Ala Thr Val Val Leu Asp Leu Ser		
	370	375 380
Met Pro Thr Met Ser Ile Phe Leu Gly Met Ser Tyr Lys Phe Phe Cys		
385	390	395 400
Ala Val Arg Thr Met Tyr Gln		
	405	

<210> 79
 <211> 1212
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(1212)

<223> DORLU 13.1

<400> 79

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Met Glu Thr Ala Lys Asp Asn Thr Ala Arg Thr Phe Met Glu Leu Met	
1 5 10 15	
cga gtg cca gta cag ttt tac aga acg att gga gag gat atc tac gcc	96
Arg Val Pro Val Gln Phe Tyr Arg Thr Ile Gly Glu Asp Ile Tyr Ala	
20 25 30	
cat cga tcc acg aat ccc cta aaa tcg ctt ctc ttc aag atc tat cta	144
His Arg Ser Thr Asn Pro Leu Lys Ser Leu Leu Phe Lys Ile Tyr Leu	
35 40 45	
tat gcg gga ttc ata aat ttt aat ctg ttg gta atc ggt gaa ctg gtg	192
Tyr Ala Gly Phe Ile Asn Phe Asn Leu Leu Val Ile Gly Glu Leu Val	
50 55 60	
ttc ttc tac aac tca att cag gac ttt gaa acc att cga ttg gcc atc	240
Phe Phe Tyr Asn Ser Ile Gln Asp Phe Glu Thr Ile Arg Leu Ala Ile	
65 70 75 80	
gcg gtg gct cca tgt atc gga ttt tct ctg gtt gct gat ttt aaa caa	288
Ala Val Ala Pro Cys Ile Gly Phe Ser Leu Val Ala Asp Phe Lys Gln	
85 90 95	
gct gcc atg att aga ggc aag aaa aca cta att atg cta ctc gat gat	336
Ala Ala Met Ile Arg Gly Lys Lys Thr Leu Ile Met Leu Leu Asp Asp	
100 105 110	
ttg gag aac atg cat ccg aaa acc ctg gca aag caa atg gaa tac aaa	384
Leu Glu Asn Met His Pro Lys Thr Leu Ala Lys Gln Met Glu Tyr Lys	
115 120 125	
ttg ccg gac ttt gaa aag acc atg aaa cgt gtg atc aat ata ttc acc	432
Leu Pro Asp Phe Glu Lys Thr Met Lys Arg Val Ile Asn Ile Phe Thr	
130 135 140	
ttt ctc tgc ttg gcc tat acg act acg ttc tcc ttt tat ccg gcc atc	480
Phe Leu Cys Leu Ala Tyr Thr Thr Thr Phe Ser Phe Tyr Pro Ala Ile	
145 150 155 160	
aag gca tcc gtg aaa ttt aat ttc ttg ggc tac gac acc ttt gat cga	528
Lys Ala Ser Val Lys Phe Asn Phe Leu Gly Tyr Asp Thr Phe Asp Arg	
165 170 175	
aat ttt ggt ttc ctc atc tgg ttt ccc ttc gat gca aca agg aat aat	576

Asn Phe Gly Phe Leu Ile Trp Phe Pro Phe Asp Ala Thr Arg Asn Asn	
180 185 190	
ttg ata tac tgg atc atg tac tgg gac ata gcc cat ggg gcc tat cta	624
Leu Ile Tyr Trp Ile Met Tyr Trp Asp Ile Ala His Gly Ala Tyr Leu	
195 200 205	
ggg ggt att gct ttt ctc tgc gcc gat ctt ttg ctc gtc gta gtc att	672
Ala Gly Ile Ala Phe Leu Cys Ala Asp Leu Leu Leu Val Val Val Ile	
210 215 220	
acc cag att tgt atg cac ttt aac tat ata tct atg cga tta gag gat	720
Thr Gln Ile Cys Met His Phe Asn Tyr Ile Ser Met Arg Leu Glu Asp	
225 230 235 240	
cat cca tgt aat tcg aat gag gac aaa gag aat ata gag ttt ctt att	768
His Pro Cys Asn Ser Asn Glu Asp Lys Glu Asn Ile Glu Phe Leu Ile	
245 250 255	
ggc att atc aga tac cat gac aag tgc ctt aaa cta tgc gaa cat gtc	816
Gly Ile Ile Arg Tyr His Asp Lys Cys Leu Lys Leu Cys Glu His Val	
260 265 270	
aac gat ctg tat agt ttc tct ttg ctg ctt aat ttc ctt atg gca tcc	864
Asn Asp Leu Tyr Ser Phe Ser Leu Leu Leu Asn Phe Leu Met Ala Ser	
275 280 285	
atg cag att tgt ttc ata gcc ttt cag gtc acc gaa tca aca gtg gaa	912
Met Gln Ile Cys Phe Ile Ala Phe Gln Val Thr Glu Ser Thr Val Glu	
290 295 300	
gtg att att att tac tgc att ttt ttg atg acc tcg atg gtt cag gta	960
Val Ile Ile Ile Tyr Cys Ile Phe Leu Met Thr Ser Met Val Gln Val	
305 310 315 320	
ttt atg gtg tgc tac tat ggg gat act tta att gcc gcg agc ttg aaa	1008
Phe Met Val Cys Tyr Tyr Gly Asp Thr Leu Ile Ala Ala Ser Leu Lys	
325 330 335	
gtg ggc gat gcc gct tac aac caa aag tgg ttt cag tgc agc aaa tcc	1056
Val Gly Asp Ala Ala Tyr Asn Gln Lys Trp Phe Gln Cys Ser Lys Ser	
340 345 350	
tat tgc acc atg ttg aag ttg cta atc atg agg agt cag aaa cca gct	1104
Tyr Cys Thr Met Leu Lys Leu Leu Ile Met Arg Ser Gln Lys Pro Ala	
355 360 365	
tca ata aga ccg ccg act ttt ccc ccc ata tcc ttg gtt acc tat atg	1152

Ser Ile Arg Pro Pro Thr Phe Pro Pro Ile Ser Leu Val Thr Tyr Met
 370 375 380

aag gtc atc agc atg tcg tat caa ttt ttt gcc tta ctt aga acc aca 1200
 Lys Val Ile Ser Met Ser Tyr Gln Phe Phe Ala Leu Leu Arg Thr Thr
 385 390 395 400

tac agc aat aat 1212
 Tyr Ser Asn Asn

<210> 80
 <211> 404
 <212> PRT
 <213> Drosophila melanogaster

<400> 80
 Met Glu Thr Ala Lys Asp Asn Thr Ala Arg Thr Phe Met Glu Leu Met
 1 5 10 15

Arg Val Pro Val Gln Phe Tyr Arg Thr Ile Gly Glu Asp Ile Tyr Ala
 20 25 30

His Arg Ser Thr Asn Pro Leu Lys Ser Leu Leu Phe Lys Ile Tyr Leu
 35 40 45

Tyr Ala Gly Phe Ile Asn Phe Asn Leu Leu Val Ile Gly Glu Leu Val
 50 55 60

Phe Phe Tyr Asn Ser Ile Gln Asp Phe Glu Thr Ile Arg Leu Ala Ile
 65 70 75 80

Ala Val Ala Pro Cys Ile Gly Phe Ser Leu Val Ala Asp Phe Lys Gln
 85 90 95

Ala Ala Met Ile Arg Gly Lys Lys Thr Leu Ile Met Leu Leu Asp Asp
 100 105 110

Leu Glu Asn Met His Pro Lys Thr Leu Ala Lys Gln Met Glu Tyr Lys
 115 120 125

Leu Pro Asp Phe Glu Lys Thr Met Lys Arg Val Ile Asn Ile Phe Thr
 130 135 140

Phe Leu Cys Leu Ala Tyr Thr Thr Thr Phe Ser Phe Tyr Pro Ala Ile
 145 150 155 160

Lys Ala Ser Val Lys Phe Asn Phe Leu Gly Tyr Asp Thr Phe Asp Arg

	165		170		175
Asn Phe Gly Phe Leu Ile Trp Phe Pro Phe Asp Ala Thr Arg Asn Asn	180	185	190		
Leu Ile Tyr Trp Ile Met Tyr Trp Asp Ile Ala His Gly Ala Tyr Leu	195	200	205		
Ala Gly Ile Ala Phe Leu Cys Ala Asp Leu Leu Leu Val Val Val Ile	210	215	220		
Thr Gln Ile Cys Met His Phe Asn Tyr Ile Ser Met Arg Leu Glu Asp	225	230	235	240	
His Pro Cys Asn Ser Asn Glu Asp Lys Glu Asn Ile Glu Phe Leu Ile	245	250	255		
Gly Ile Ile Arg Tyr His Asp Lys Cys Leu Lys Leu Cys Glu His Val	260	265	270		
Asn Asp Leu Tyr Ser Phe Ser Leu Leu Leu Asn Phe Leu Met Ala Ser	275	280	285		
Met Gln Ile Cys Phe Ile Ala Phe Gln Val Thr Glu Ser Thr Val Glu	290	295	300		
Val Ile Ile Ile Tyr Cys Ile Phe Leu Met Thr Ser Met Val Gln Val	305	310	315	320	
Phe Met Val Cys Tyr Tyr Gly Asp Thr Leu Ile Ala Ala Ser Leu Lys	325	330	335		
Val Gly Asp Ala Ala Tyr Asn Gln Lys Trp Phe Gln Cys Ser Lys Ser	340	345	350		
Tyr Cys Thr Met Leu Lys Leu Leu Ile Met Arg Ser Gln Lys Pro Ala	355	360	365		
Ser Ile Arg Pro Pro Thr Phe Pro Pro Ile Ser Leu Val Thr Tyr Met	370	375	380		
Lys Val Ile Ser Met Ser Tyr Gln Phe Phe Ala Leu Leu Arg Thr Thr	385	390	395	400	
Tyr Ser Asn Asn					

<210> 81
 <211> 1179
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(1179)
 <223> DORLU 14.1

<400> 81
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 Met Glu Pro Val Gln Tyr Ser Tyr Glu Asp Phe Ala Arg Leu Pro Thr
 1 5 10 15
 acg gtg ttc tgg atc atg ggc tac gac atg ctg ggc gtt ccg aag acc 96
 Thr Val Phe Trp Ile Met Gly Tyr Asp Met Leu Gly Val Pro Lys Thr
 20 25 30
 cgc tct cgc agg ata cta tac tgg ata tat cgt ttc ctc tgt ctc gcc 144
 Arg Ser Arg Arg Ile Leu Tyr Trp Ile Tyr Arg Phe Leu Cys Leu Ala
 35 40 45
 agc cat ggg gtc tgt gta gga gtc atg gta ttt cgt atg gtg gag gca 192
 Ser His Gly Val Cys Val Gly Val Met Val Phe Arg Met Val Glu Ala
 50 55 60
 aag acc att gac aat gtt tcg ctg atc atg cgg tat gcc act ctg gtc 240
 Lys Thr Ile Asp Asn Val Ser Leu Ile Met Arg Tyr Ala Thr Leu Val
 65 70 75 80
 acc tat atc atc aac tcg gat acg aaa ttc gca act gtc tta caa agg 288
 Thr Tyr Ile Ile Asn Ser Asp Thr Lys Phe Ala Thr Val Leu Gln Arg
 85 90 95
 agt gca att caa agt cta aac tca aaa ctg gcc gaa cta tat ccg aag 336
 Ser Ala Ile Gln Ser Leu Asn Ser Lys Leu Ala Glu Leu Tyr Pro Lys
 100 105 110
 acc acg ctg gac agg atc tat cac cgg gtg aat gat cac tat tgg acc 384
 Thr Thr Leu Asp Arg Ile Tyr His Arg Val Asn Asp His Tyr Trp Thr
 115 120 125
 aag tca ttt gta tat ttg gtt att atc tac att ggt tcg tcg att atg 432
 Lys Ser Phe Val Tyr Leu Val Ile Ile Tyr Ile Gly Ser Ser Ile Met
 130 135 140

ggt ggt att gga ccg att att acg tgc att ata gct tac ttc acg cac	480
Val Val Ile Gly Pro Ile Ile Thr Ser Ile Ile Ala Tyr Phe Thr His	
145 150 155 160	
aac gtt ttc acc tac atg cac tgc tat ccg tac ttt ttg tat gat cct	528
Asn Val Phe Thr Tyr Met His Cys Tyr Pro Tyr Phe Leu Tyr Asp Pro	
165 170 175	
gag aag gat ccg gtt tgg atc tac atc agc atc tat gct ctg gaa tgg	576
Glu Lys Asp Pro Val Trp Ile Tyr Ile Ser Ile Tyr Ala Leu Glu Trp	
180 185 190	
ttg cac agc aca cag atg gtc att tgc aac att ggc gcg gat atc tgg	624
Leu His Ser Thr Gln Met Val Ile Ser Asn Ile Gly Ala Asp Ile Trp	
195 200 205	
ctg ctg tac ttt cag gtg cag ata aat ctc cac ttc agg ggc att ata	672
Leu Leu Tyr Phe Gln Val Gln Ile Asn Leu His Phe Arg Gly Ile Ile	
210 215 220	
cga tca ctg gcg gat cac aag ccc agt gtg aag cac gac cag gag gac	720
Arg Ser Leu Ala Asp His Lys Pro Ser Val Lys His Asp Gln Glu Asp	
225 230 235 240	
agg aaa ttc att gcg aaa att gtc gac aag cag gtg cac ctg gtc agt	768
Arg Lys Phe Ile Ala Lys Ile Val Asp Lys Gln Val His Leu Val Ser	
245 250 255	
ttg caa aac gat ctg aat ggt atc ttt gga aaa tgc ctg ctt cta agc	816
Leu Gln Asn Asp Leu Asn Gly Ile Phe Gly Lys Ser Leu Leu Leu Ser	
260 265 270	
ctg ctg acc acc gca gcg gtt atc tgc acg gtg gcg gtg tac act ctg	864
Leu Leu Thr Thr Ala Ala Val Ile Cys Thr Val Ala Val Tyr Thr Leu	
275 280 285	
att cag ggt ccc acc ttg gag ggc ttc acc tat gtg atc ttc atc ggg	912
Ile Gln Gly Pro Thr Leu Glu Gly Phe Thr Tyr Val Ile Phe Ile Gly	
290 295 300	
act tct gtg atg cag gtc tac ctg gtg tgc tat tac ggt cag caa gtt	960
Thr Ser Val Met Gln Val Tyr Leu Val Cys Tyr Tyr Gly Gln Gln Val	
305 310 315 320	
ctc gac ttg gtg gag cgc gag gtg gcc cac gcc gtg tac aat cat gat	1008
Leu Asp Leu Val Glu Arg Glu Val Ala His Ala Val Tyr Asn His Asp	
325 330 335	

ttt cac gat gct tct ata gcg tac aag agg tac ctg ctc ata atc att 1056
Phe His Asp Ala Ser Ile Ala Tyr Lys Arg Tyr Leu Leu Ile Ile Ile
340 345 350

atc agg gcg cag cag ccc gtg gaa ctt aat gcc atg ggc tac ctg tcc 1104
Ile Arg Ala Gln Gln Pro Val Glu Leu Asn Ala Met Gly Tyr Leu Ser
355 360 365

att tcg ctg gac acc ttt aaa cag ctg atg agc gtc tcc tac cgg gtt 1152
Ile Ser Leu Asp Thr Phe Lys Gln Leu Met Ser Val Ser Tyr Arg Val
370 375 380

ata acc atg ctc atg cag atg att cag 1179
Ile Thr Met Leu Met Gln Met Ile Gln
385 390

<210> 82

<211> 393

<212> PRT

<213> *Drosophila melanogaster*

<400> 82

Met Glu Pro Val Gln Tyr Ser Tyr Glu Asp Phe Ala Arg Leu Pro Thr
1 5 10 15

Thr Val Phe Trp Ile Met Gly Tyr Asp Met Leu Gly Val Pro Lys Thr
20 25 30

Arg Ser Arg Arg Ile Leu Tyr Trp Ile Tyr Arg Phe Leu Cys Leu Ala
35 40 45

Ser His Gly Val Cys Val Gly Val Met Val Phe Arg Met Val Glu Ala
50 55 60

Lys Thr Ile Asp Asn Val Ser Leu Ile Met Arg Tyr Ala Thr Leu Val
65 70 75 80

Thr Tyr Ile Ile Asn Ser Asp Thr Lys Phe Ala Thr Val Leu Gln Arg
85 90 95

Ser Ala Ile Gln Ser Leu Asn Ser Lys Leu Ala Glu Leu Tyr Pro Lys
100 105 110

Thr Thr Leu Asp Arg Ile Tyr His Arg Val Asn Asp His Tyr Trp Thr
115 120 125

Lys Ser Phe Val Tyr Leu Val Ile Ile Tyr Ile Gly Ser Ser Ile Met

130	135	140
Val Val Ile Gly Pro Ile Ile Thr Ser Ile Ile Ala Tyr Phe Thr His		
145	150	155 160
Asn Val Phe Thr Tyr Met His Cys Tyr Pro Tyr Phe Leu Tyr Asp Pro		
	165	170 175
Glu Lys Asp Pro Val Trp Ile Tyr Ile Ser Ile Tyr Ala Leu Glu Trp		
	180	185 190
Leu His Ser Thr Gln Met Val Ile Ser Asn Ile Gly Ala Asp Ile Trp		
	195	200 205
Leu Leu Tyr Phe Gln Val Gln Ile Asn Leu His Phe Arg Gly Ile Ile		
	210	215 220
Arg Ser Leu Ala Asp His Lys Pro Ser Val Lys His Asp Gln Glu Asp		
	225	230 235 240
Arg Lys Phe Ile Ala Lys Ile Val Asp Lys Gln Val His Leu Val Ser		
	245	250 255
Leu Gln Asn Asp Leu Asn Gly Ile Phe Gly Lys Ser Leu Leu Leu Ser		
	260	265 270
Leu Leu Thr Thr Ala Ala Val Ile Cys Thr Val Ala Val Tyr Thr Leu		
	275	280 285
Ile Gln Gly Pro Thr Leu Glu Gly Phe Thr Tyr Val Ile Phe Ile Gly		
	290	295 300
Thr Ser Val Met Gln Val Tyr Leu Val Cys Tyr Tyr Gly Gln Gln Val		
	305	310 315 320
Leu Asp Leu Val Glu Arg Glu Val Ala His Ala Val Tyr Asn His Asp		
	325	330 335
Phe His Asp Ala Ser Ile Ala Tyr Lys Arg Tyr Leu Leu Ile Ile Ile		
	340	345 350
Ile Arg Ala Gln Gln Pro Val Glu Leu Asn Ala Met Gly Tyr Leu Ser		
	355	360 365
Ile Ser Leu Asp Thr Phe Lys Gln Leu Met Ser Val Ser Tyr Arg Val		
	370	375 380
Ile Thr Met Leu Met Gln Met Ile Gln		

<210> 83
 <211> 1134
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
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 <222> (1)..(1134)
 <223> DORLU 15.1

<400> 83

atg gac gcc agc tac ttt gcc gtc cag aga aga gct ctg gaa ata gtt	48
Met Asp Ala Ser Tyr Phe Ala Val Gln Arg Arg Ala Leu Glu Ile Val	
1 5 10 15	
gga ttc gat ccc agt act ccg caa ctg agt ctg aaa cat ccc atc tgg	96
Gly Phe Asp Pro Ser Thr Pro Gln Leu Ser Leu Lys His Pro Ile Trp	
20 25 30	
gcc ggg att ctc atc ctg tcc ttg atc tct cac aac tgg ccc atg gta	144
Ala Gly Ile Leu Ile Leu Ser Leu Ile Ser His Asn Trp Pro Met Val	
35 40 45	
gtc tat gcc ctg cag gat ctc tcc gac ttg acc cgt ctg acg gac aac	192
Val Tyr Ala Leu Gln Asp Leu Ser Asp Leu Thr Arg Leu Thr Asp Asn	
50 55 60	
ttt gcg gtg ttt atg caa gga tca cag agc acc ttc aag ttc ctg gtc	240
Phe Ala Val Phe Met Gln Gly Ser Gln Ser Thr Phe Lys Phe Leu Val	
65 70 75 80	
atg atg gcg aaa cga agg cgc att gga tcg ttg att cac cgt ttg cat	288
Met Met Ala Lys Arg Arg Arg Ile Gly Ser Leu Ile His Arg Leu His	
85 90 95	
aag cta aac cag gcg gcc agt gcc acg ccc aat cac ctg gag aag atc	336
Lys Leu Asn Gln Ala Ala Ser Ala Thr Pro Asn His Leu Glu Lys Ile	
100 105 110	
gag agg gaa aac caa ctg gat agg tat gtc gcc agg tcc ttt aga aat	384
Glu Arg Glu Asn Gln Leu Asp Arg Tyr Val Ala Arg Ser Phe Arg Asn	
115 120 125	
gcc gcc tac gga gtg att tgt gcc tcg gcc ata gcg ccc atg ttg ctt	432

Ala Ala Tyr Gly Val Ile Cys Ala Ser Ala Ile Ala Pro Met Leu Leu	
130	135 140
ggc ctg tgg gga tat gtg gag acg ggt gta ttt acc ccg acc aca ccc	480
Gly Leu Trp Gly Tyr Val Glu Thr Gly Val Phe Thr Pro Thr Thr Pro	
145	150 155 160
atg gag ttc aac ttc tgg ctg gac gag cga aag cct cac ttt tat tgg	528
Met Glu Phe Asn Phe Trp Leu Asp Glu Arg Lys Pro His Phe Tyr Trp	
	165 170 175
ccc atc tac gtt tgg ggc gta ctg ggc gtg gca gct gcc gcc tgg ttg	576
Pro Ile Tyr Val Trp Gly Val Leu Gly Val Ala Ala Ala Ala Trp Leu	
	180 185 190
gcc att gca acg gac acc ctg ttc tcc tgg ctg act cac aat gtg gtg	624
Ala Ile Ala Thr Asp Thr Leu Phe Ser Trp Leu Thr His Asn Val Val	
	195 200 205
att cag ttc caa cta ctg gag ctt gtt ctc gaa gag aag gat ctg aat	672
Ile Gln Phe Gln Leu Leu Glu Leu Val Leu Glu Glu Lys Asp Leu Asn	
	210 215 220
ggc gga gac tct cgc ctg acc ggg ttt gtt agt cgt cat cgt ata gct	720
Gly Gly Asp Ser Arg Leu Thr Gly Phe Val Ser Arg His Arg Ile Ala	
225	230 235 240
ctg gat ttg gcc aag gaa cta agt tcg att ttc ggg gag atc gtc ttt	768
Leu Asp Leu Ala Lys Glu Leu Ser Ser Ile Phe Gly Glu Ile Val Phe	
	245 250 255
gtg aaa tac atg ctc agt tac ctg caa ctc tgc atg ttg gcc ttt cgc	816
Val Lys Tyr Met Leu Ser Tyr Leu Gln Leu Cys Met Leu Ala Phe Arg	
	260 265 270
ttc agc cgc agt ggc tgg agt gcc cag gtg cca ttt aga gcc acc ttc	864
Phe Ser Arg Ser Gly Trp Ser Ala Gln Val Pro Phe Arg Ala Thr Phe	
	275 280 285
cta gtg gcc atc atc atc caa ctg agt tcg tat tgc tat gga ggc gag	912
Leu Val Ala Ile Ile Ile Gln Leu Ser Ser Tyr Cys Tyr Gly Gly Glu	
	290 295 300
tat ata aag cag caa agt ttg gcc atc gca caa gcc gtt tat ggt caa	960
Tyr Ile Lys Gln Gln Ser Leu Ala Ile Ala Gln Ala Val Tyr Gly Gln	
305	310 315 320
atc aat tgg cca gaa atg acg cca aag aaa aga aga ctc tgg caa atg	1008

Ile Asn Trp Pro Glu Met Thr Pro Lys Lys Arg Arg Leu Trp Gln Met	
325 330 335	
gtg atc atg agg gcg cag cga ccg gct aag att ttt gga ttc atg ttc	1056
Val Ile Met Arg Ala Gln Arg Pro Ala Lys Ile Phe Gly Phe Met Phe	
340 345 350	
gtt gtg gac ttg cca ctg ctg ctt tgg gtc atc aga act gcg ggc tca	1104
Val Val Asp Leu Pro Leu Leu Trp Val Ile Arg Thr Ala Gly Ser	
355 360 365	
ttt ctg gcc atg ctt agg act ttc gag cgt	1134
Phe Leu Ala Met Leu Arg Thr Phe Glu Arg	
370 375	

<210> 84
 <211> 378
 <212> PRT
 <213> Drosophila melanogaster

<400> 84	
Met Asp Ala Ser Tyr Phe Ala Val Gln Arg Arg Ala Leu Glu Ile Val	
1 5 10 15	
Gly Phe Asp Pro Ser Thr Pro Gln Leu Ser Leu Lys His Pro Ile Trp	
20 25 30	
Ala Gly Ile Leu Ile Leu Ser Leu Ile Ser His Asn Trp Pro Met Val	
35 40 45	
Val Tyr Ala Leu Gln Asp Leu Ser Asp Leu Thr Arg Leu Thr Asp Asn	
50 55 60	
Phe Ala Val Phe Met Gln Gly Ser Gln Ser Thr Phe Lys Phe Leu Val	
65 70 75 80	
Met Met Ala Lys Arg Arg Arg Ile Gly Ser Leu Ile His Arg Leu His	
85 90 95	
Lys Leu Asn Gln Ala Ala Ser Ala Thr Pro Asn His Leu Glu Lys Ile	
100 105 110	
Glu Arg Glu Asn Gln Leu Asp Arg Tyr Val Ala Arg Ser Phe Arg Asn	
115 120 125	
Ala Ala Tyr Gly Val Ile Cys Ala Ser Ala Ile Ala Pro Met Leu Leu	
130 135 140	

Gly	Leu	Trp	Gly	Tyr	Val	Glu	Thr	Gly	Val	Phe	Thr	Pro	Thr	Thr	Pro	145	150	155	160
Met	Glu	Phe	Asn	Phe	Trp	Leu	Asp	Glu	Arg	Lys	Pro	His	Phe	Tyr	Trp	165	170	175	
Pro	Ile	Tyr	Val	Trp	Gly	Val	Leu	Gly	Val	Ala	Ala	Ala	Ala	Trp	Leu	180	185	190	
Ala	Ile	Ala	Thr	Asp	Thr	Leu	Phe	Ser	Trp	Leu	Thr	His	Asn	Val	Val	195	200	205	
Ile	Gln	Phe	Gln	Leu	Leu	Glu	Leu	Val	Leu	Glu	Glu	Lys	Asp	Leu	Asn	210	215	220	
Gly	Gly	Asp	Ser	Arg	Leu	Thr	Gly	Phe	Val	Ser	Arg	His	Arg	Ile	Ala	225	230	235	240
Leu	Asp	Leu	Ala	Lys	Glu	Leu	Ser	Ser	Ile	Phe	Gly	Glu	Ile	Val	Phe	245	250	255	
Val	Lys	Tyr	Met	Leu	Ser	Tyr	Leu	Gln	Leu	Cys	Met	Leu	Ala	Phe	Arg	260	265	270	
Phe	Ser	Arg	Ser	Gly	Trp	Ser	Ala	Gln	Val	Pro	Phe	Arg	Ala	Thr	Phe	275	280	285	
Leu	Val	Ala	Ile	Ile	Ile	Gln	Leu	Ser	Ser	Tyr	Cys	Tyr	Gly	Gly	Glu	290	295	300	
Tyr	Ile	Lys	Gln	Gln	Ser	Leu	Ala	Ile	Ala	Gln	Ala	Val	Tyr	Gly	Gln	305	310	315	320
Ile	Asn	Trp	Pro	Glu	Met	Thr	Pro	Lys	Lys	Arg	Arg	Leu	Trp	Gln	Met	325	330	335	
Val	Ile	Met	Arg	Ala	Gln	Arg	Pro	Ala	Lys	Ile	Phe	Gly	Phe	Met	Phe	340	345	350	
Val	Val	Asp	Leu	Pro	Leu	Leu	Leu	Trp	Val	Ile	Arg	Thr	Ala	Gly	Ser	355	360	365	
Phe	Leu	Ala	Met	Leu	Arg	Thr	Phe	Glu	Arg							370	375		

<210> 85
 <211> 1065
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1065)
 <223> DORLU 16.1

<400> 85

atg gaa aaa cta cgt tcc tat gag gat ttc atc ttc atg gcc aac atg	48
Met Glu Lys Leu Arg Ser Tyr Glu Asp Phe Ile Phe Met Ala Asn Met	
1 5 10 15	

atg ttc aag acc ctt ggc tac gat cta ttc cat aca ccc aaa ccc tgg	96
Met Phe Lys Thr Leu Gly Tyr Asp Leu Phe His Thr Pro Lys Pro Trp	
20 25 30	

tgg cgc tat ctg ctt gtg cga gga tac ttc gtt ttg tgc acg atc agc	144
Trp Arg Tyr Leu Leu Val Arg Gly Tyr Phe Val Leu Cys Thr Ile Ser	
35 40 45	

aac ttt tac gag gct tcc atg gtg acg aca agg ata att gag tgg gaa	192
Asn Phe Tyr Glu Ala Ser Met Val Thr Thr Arg Ile Ile Glu Trp Glu	
50 55 60	

tcc ttg gcc gga agt ccc tcc aaa ata atg cga cag ggt ctg cac ttc	240
Ser Leu Ala Gly Ser Pro Ser Lys Ile Met Arg Gln Gly Leu His Phe	
65 70 75 80	

ttt tac atg ttg agt agc caa ttg aaa ttt atc aca ttc atg ata aat	288
Phe Tyr Met Leu Ser Ser Gln Leu Lys Phe Ile Thr Phe Met Ile Asn	
85 90 95	

cgc aaa cgc cta ctg cag ctg agc cat cgt ttg aaa gag ttg tat cct	336
Arg Lys Arg Leu Leu Gln Leu Ser His Arg Leu Lys Glu Leu Tyr Pro	
100 105 110	

cat aaa gag caa aat caa agg aag tac gag gtg aat aaa tac tac cta	384
His Lys Glu Gln Asn Gln Arg Lys Tyr Glu Val Asn Lys Tyr Tyr Leu	
115 120 125	

tcc tgt tcc acg cgc aat gtt ttg tac gtg tac tac ttt gta atg gtc	432
Ser Cys Ser Thr Arg Asn Val Leu Tyr Val Tyr Tyr Phe Val Met Val	
130 135 140	

gtc atg gca ctg gaa ccc ctc gtt cag tcg tgc att atc cag ttc ata	480
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Val Met Ala Leu Glu Pro Leu Val Gln Ser Cys Ile Ile Gln Phe Ile	
145	150 155 160
gtg aat gtg agc ctg ggc aca gat ctg tgg atg atg tgc gtc tca agc	528
Val Asn Val Ser Leu Gly Thr Asp Leu Trp Met Met Cys Val Ser Ser	
165	170 175
caa ata tcg atg cac ttg ggc tat ctg gcc aat atg ttg gcc tcc att	576
Gln Ile Ser Met His Leu Gly Tyr Leu Ala Asn Met Leu Ala Ser Ile	
180	185 190
cga cca agt cca gaa acg gaa caa caa gac tgt gac ttc ttg gcc agc	624
Arg Pro Ser Pro Glu Thr Glu Gln Gln Asp Cys Asp Phe Leu Ala Ser	
195	200 205
att ata aag aga cat caa cta atg atc agg ctt caa aag gac gtg aac	672
Ile Ile Lys Arg His Gln Leu Met Ile Arg Leu Gln Lys Asp Val Asn	
210	215 220
tat gtt ttt gga ctc tta ttg gca tct aat ctg ttt acc aca tcc tgt	720
Tyr Val Phe Gly Leu Leu Leu Ala Ser Asn Leu Phe Thr Thr Ser Cys	
225	230 235 240
tta ctt tgc tgc atg gcg tac tat acc gtc gtc gaa ggt ttc aat tgg	768
Leu Leu Cys Cys Met Ala Tyr Tyr Thr Val Val Glu Gly Phe Asn Trp	
245	250 255
gag ggc att tcc tat atg atg ctc ttt gct agt gta gct gcc cag ttc	816
Glu Gly Ile Ser Tyr Met Met Leu Phe Ala Ser Val Ala Ala Gln Phe	
260	265 270
tac gtt gtc agc tca cac gga caa atg tta ata gat ttg agt aca aat	864
Tyr Val Val Ser Ser His Gly Gln Met Leu Ile Asp Leu Ser Thr Asn	
275	280 285
tta gcc aag gct gcc ttt gaa agc aag tgg tat gaa gga tct ttg cga	912
Leu Ala Lys Ala Ala Phe Glu Ser Lys Trp Tyr Glu Gly Ser Leu Arg	
290	295 300
tac aaa aag gag ata ctc att cta atg gca cag gct caa cga cct ttg	960
Tyr Lys Lys Glu Ile Leu Ile Leu Met Ala Gln Ala Gln Arg Pro Leu	
305	310 315 320
gag att tca gcc agg gga gta att atc ata tcc ctc gac acc ttt aaa	1008
Glu Ile Ser Ala Arg Gly Val Ile Ile Ile Ser Leu Asp Thr Phe Lys	
325	330 335
ata ttg atg acc atc aca tac aga ttt ttc gcg gtt ata cga caa act	1056

Ile Leu Met Thr Ile Thr Tyr Arg Phe Phe Ala Val Ile Arg Gln Thr
 340 345 350

gta gaa aag
 Val Glu Lys
 355

1065

<210> 86
 <211> 355
 <212> PRT
 <213> Drosophila melanogaster

<400> 86
 Met Glu Lys Leu Arg Ser Tyr Glu Asp Phe Ile Phe Met Ala Asn Met
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Met Phe Lys Thr Leu Gly Tyr Asp Leu Phe His Thr Pro Lys Pro Trp
 20 25 30

Trp Arg Tyr Leu Leu Val Arg Gly Tyr Phe Val Leu Cys Thr Ile Ser
 35 40 45

Asn Phe Tyr Glu Ala Ser Met Val Thr Thr Arg Ile Ile Glu Trp Glu
 50 55 60

Ser Leu Ala Gly Ser Pro Ser Lys Ile Met Arg Gln Gly Leu His Phe
 65 70 75 80

Phe Tyr Met Leu Ser Ser Gln Leu Lys Phe Ile Thr Phe Met Ile Asn
 85 90 95

Arg Lys Arg Leu Leu Gln Leu Ser His Arg Leu Lys Glu Leu Tyr Pro
 100 105 110

His Lys Glu Gln Asn Gln Arg Lys Tyr Glu Val Asn Lys Tyr Tyr Leu
 115 120 125

Ser Cys Ser Thr Arg Asn Val Leu Tyr Val Tyr Tyr Phe Val Met Val
 130 135 140

Val Met Ala Leu Glu Pro Leu Val Gln Ser Cys Ile Ile Gln Phe Ile
 145 150 155 160

Val Asn Val Ser Leu Gly Thr Asp Leu Trp Met Met Cys Val Ser Ser
 165 170 175

Gln Ile Ser Met His Leu Gly Tyr Leu Ala Asn Met Leu Ala Ser Ile

180	185	190
Arg Pro Ser Pro Glu Thr Glu Gln Gln Asp Cys Asp Phe Leu Ala Ser		
195	200	205
Ile Ile Lys Arg His Gln Leu Met Ile Arg Leu Gln Lys Asp Val Asn		
210	215	220
Tyr Val Phe Gly Leu Leu Leu Ala Ser Asn Leu Phe Thr Thr Ser Cys		
225	230	235 240
Leu Leu Cys Cys Met Ala Tyr Tyr Thr Val Val Glu Gly Phe Asn Trp		
	245	250 255
Glu Gly Ile Ser Tyr Met Met Leu Phe Ala Ser Val Ala Ala Gln Phe		
	260	265 270
Tyr Val Val Ser Ser His Gly Gln Met Leu Ile Asp Leu Ser Thr Asn		
	275	280 285
Leu Ala Lys Ala Ala Phe Glu Ser Lys Trp Tyr Glu Gly Ser Leu Arg		
	290	295 300
Tyr Lys Lys Glu Ile Leu Ile Leu Met Ala Gln Ala Gln Arg Pro Leu		
305	310	315 320
Glu Ile Ser Ala Arg Gly Val Ile Ile Ile Ser Leu Asp Thr Phe Lys		
	325	330 335
Ile Leu Met Thr Ile Thr Tyr Arg Phe Phe Ala Val Ile Arg Gln Thr		
	340	345 350
Val Glu Lys		
355		

<210> 87
 <211> 1272
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1272)
 <223> DORLU 22.1

<400> 87

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Met Leu Thr Asp Lys Phe Leu Arg Leu Gln Ser Ala Leu Phe Arg Leu	
1 5 10 15	
ctc gga ctc gaa ttg ttg cac gag cag gat gtt ggc cat cga tat cct	96
Leu Gly Leu Glu Leu Leu His Glu Gln Asp Val Gly His Arg Tyr Pro	
20 25 30	
tgg cgc agc atc tgc tgc att ctc tcg gtg gcc agt ttc atg ccc ctg	144
Trp Arg Ser Ile Cys Cys Ile Leu Ser Val Ala Ser Phe Met Pro Leu	
35 40 45	
acc att gcg ttt ggc ctg caa aac gtc caa aat gtg gag caa tta acc	192
Thr Ile Ala Phe Gly Leu Gln Asn Val Gln Asn Val Glu Gln Leu Thr	
50 55 60	
gac tca ctc tgc tcg gtt ctc gtg gat ttg ctg gcc ctg tgc aaa atc	240
Asp Ser Leu Cys Ser Val Leu Val Asp Leu Leu Ala Leu Cys Lys Ile	
65 70 75 80	
ggg ctt ttc ctt tgg ctt tac aag gac ttc aag ttc cta ata ggg cag	288
Gly Leu Phe Leu Trp Leu Tyr Lys Asp Phe Lys Phe Leu Ile Gly Gln	
85 90 95	
ttc tat tgt gtt ttg caa acg gaa acc cac acc gct gtc gct gaa atg	336
Phe Tyr Cys Val Leu Gln Thr Glu Thr His Thr Ala Val Ala Glu Met	
100 105 110	
ata gtg acc agg gaa agt cgt cgg gat cag ttc atc agt gct atg tat	384
Ile Val Thr Arg Glu Ser Arg Arg Asp Gln Phe Ile Ser Ala Met Tyr	
115 120 125	
gcc tac tgt ttc att acg gct ggc ctt tcg gcc tgc ctg atg tcc cct	432
Ala Tyr Cys Phe Ile Thr Ala Gly Leu Ser Ala Cys Leu Met Ser Pro	
130 135 140	
cta tcc atg ctg att agc tac cac gaa cag gtg aat tgc agc cga aat	480
Leu Ser Met Leu Ile Ser Tyr His Glu Gln Val Asn Cys Ser Arg Asn	
145 150 155 160	
ttc cat ttc cca gtg tgt aag aaa aag tac tgc tta ata tcc aga ata	528
Phe His Phe Pro Val Cys Lys Lys Lys Tyr Cys Leu Ile Ser Arg Ile	
165 170 175	
tta aga tac agt ttc tgc aga tat ccc tgg gac aat atg aag ctg tcc	576
Leu Arg Tyr Ser Phe Cys Arg Tyr Pro Trp Asp Asn Met Lys Leu Ser	
180 185 190	

aac tac atc att tcc tat ttc tgg aat gtg tgt gct gca ttg ggc gtg	624
Asn Tyr Ile Ile Ser Tyr Phe Trp Asn Val Cys Ala Ala Leu Gly Val	
195 200 205	
gca ctg ccc acc gtt tgt gtg gac aca ctg ttc tgt tct ctg agc cat	672
Ala Leu Pro Thr Val Cys Val Asp Thr Leu Phe Cys Ser Leu Ser His	
210 215 220	
aat ctc tgt gcc cta ttc cag att gcc agg cac aaa atg atg cac ttt	720
Asn Leu Cys Ala Leu Phe Gln Ile Ala Arg His Lys Met Met His Phe	
225 230 235 240	
gag ggc aga aat acc aaa gag act cat gag aac tta aag cac gtg ttt	768
Glu Gly Arg Asn Thr Lys Glu Thr His Glu Asn Leu Lys His Val Phe	
245 250 255	
caa cta tat gcg ttg tgt ttg aac ctg gcc cat ttc tta aac gaa tat	816
Gln Leu Tyr Ala Leu Cys Leu Asn Leu Gly His Phe Leu Asn Glu Tyr	
260 265 270	
ttc aga ccg ctc atc tgc cag ttt gtg gca gcc tca ctg cac ttg tgt	864
Phe Arg Pro Leu Ile Cys Gln Phe Val Ala Ala Ser Leu His Leu Cys	
275 280 285	
gtc ctg tgc tac caa ctg tct gcc aat atc ctg cag cca gcg tta ctc	912
Val Leu Cys Tyr Gln Leu Ser Ala Asn Ile Leu Gln Pro Ala Leu Leu	
290 295 300	
ttc tat gcc gca ttt acg gca gca gtt gtt ggc cag gtg tct ata tac	960
Phe Tyr Ala Ala Phe Thr Ala Ala Val Val Gly Gln Val Ser Ile Tyr	
305 310 315 320	
tgc ttc tgc gga tcg agc atc cat tcg gag tgt cag cta ttt ggc cag	1008
Cys Phe Cys Gly Ser Ser Ile His Ser Glu Cys Gln Leu Phe Gly Gln	
325 330 335	
gcc atc tac gag tcc agc tgg ccc cat ctg ctg cag gaa aac ctg cag	1056
Ala Ile Tyr Glu Ser Ser Trp Pro His Leu Leu Gln Glu Asn Leu Gln	
340 345 350	
ctt gta agc tcc tta aaa att gcc atg atg cga tcg agt ttg gga tgt	1104
Leu Val Ser Ser Leu Lys Ile Ala Met Met Arg Ser Ser Leu Gly Cys	
355 360 365	
ccc atc gat ggt tac ttc ttc gag gcc aat cgg gag acg ctc atc acg	1152
Pro Ile Asp Gly Tyr Phe Phe Glu Ala Asn Arg Glu Thr Leu Ile Thr	
370 375 380	

atc cct ggc cta gct ttc cgg gct ttc att att cag tgg ttc agt cgt 1200
 Ile Pro Gly Leu Ala Phe Arg Ala Phe Ile Ile Gln Trp Phe Ser Arg
 385 390 395 400

tcg ggt ttg ttt aac tcc gga aat att tac aat tat gct tta agc cgg 1248
 Ser Gly Leu Phe Asn Ser Gly Asn Ile Tyr Asn Tyr Ala Leu Ser Arg
 405 410 415

tgt tgt tac agc cag ttg gct aat 1272
 Cys Cys Tyr Ser Gln Leu Ala Asn
 420

<210> 88

<211> 424

<212> PRT

<213> *Drosophila melanogaster*

<400> 88

Met Leu Thr Asp Lys Phe Leu Arg Leu Gln Ser Ala Leu Phe Arg Leu
 1 5 10 15

Leu Gly Leu Glu Leu Leu His Glu Gln Asp Val Gly His Arg Tyr Pro
 20 25 30

Trp Arg Ser Ile Cys Cys Ile Leu Ser Val Ala Ser Phe Met Pro Leu
 35 40 45

Thr Ile Ala Phe Gly Leu Gln Asn Val Gln Asn Val Glu Gln Leu Thr
 50 55 60

Asp Ser Leu Cys Ser Val Leu Val Asp Leu Leu Ala Leu Cys Lys Ile
 65 70 75 80

Gly Leu Phe Leu Trp Leu Tyr Lys Asp Phe Lys Phe Leu Ile Gly Gln
 85 90 95

Phe Tyr Cys Val Leu Gln Thr Glu Thr His Thr Ala Val Ala Glu Met
 100 105 110

Ile Val Thr Arg Glu Ser Arg Arg Asp Gln Phe Ile Ser Ala Met Tyr
 115 120 125

Ala Tyr Cys Phe Ile Thr Ala Gly Leu Ser Ala Cys Leu Met Ser Pro
 130 135 140

Leu Ser Met Leu Ile Ser Tyr His Glu Gln Val Asn Cys Ser Arg Asn
 145 150 155 160

Phe	His	Phe	Pro	Val	Cys	Lys	Lys	Lys	Tyr	Cys	Leu	Ile	Ser	Arg	Ile	
				165					170					175		
Leu	Arg	Tyr	Ser	Phe	Cys	Arg	Tyr	Pro	Trp	Asp	Asn	Met	Lys	Leu	Ser	
			180					185					190			
Asn	Tyr	Ile	Ile	Ser	Tyr	Phe	Trp	Asn	Val	Cys	Ala	Ala	Leu	Gly	Val	
		195					200					205				
Ala	Leu	Pro	Thr	Val	Cys	Val	Asp	Thr	Leu	Phe	Cys	Ser	Leu	Ser	His	
	210					215					220					
Asn	Leu	Cys	Ala	Leu	Phe	Gln	Ile	Ala	Arg	His	Lys	Met	Met	His	Phe	
225					230					235					240	
Glu	Gly	Arg	Asn	Thr	Lys	Glu	Thr	His	Glu	Asn	Leu	Lys	His	Val	Phe	
			245						250					255		
Gln	Leu	Tyr	Ala	Leu	Cys	Leu	Asn	Leu	Gly	His	Phe	Leu	Asn	Glu	Tyr	
			260					265					270			
Phe	Arg	Pro	Leu	Ile	Cys	Gln	Phe	Val	Ala	Ala	Ser	Leu	His	Leu	Cys	
		275					280					285				
Val	Leu	Cys	Tyr	Gln	Leu	Ser	Ala	Asn	Ile	Leu	Gln	Pro	Ala	Leu	Leu	
	290					295					300					
Phe	Tyr	Ala	Ala	Phe	Thr	Ala	Ala	Val	Val	Gly	Gln	Val	Ser	Ile	Tyr	
305					310					315					320	
Cys	Phe	Cys	Gly	Ser	Ser	Ile	His	Ser	Glu	Cys	Gln	Leu	Phe	Gly	Gln	
			325						330					335		
Ala	Ile	Tyr	Glu	Ser	Ser	Trp	Pro	His	Leu	Leu	Gln	Glu	Asn	Leu	Gln	
			340					345					350			
Leu	Val	Ser	Ser	Leu	Lys	Ile	Ala	Met	Met	Arg	Ser	Ser	Leu	Gly	Cys	
		355					360					365				
Pro	Ile	Asp	Gly	Tyr	Phe	Phe	Glu	Ala	Asn	Arg	Glu	Thr	Leu	Ile	Thr	
	370					375					380					
Ile	Pro	Gly	Leu	Ala	Phe	Arg	Ala	Phe	Ile	Ile	Gln	Trp	Phe	Ser	Arg	
385					390					395					400	
Ser	Gly	Leu	Phe	Asn	Ser	Gly	Asn	Ile	Tyr	Asn	Tyr	Ala	Leu	Ser	Arg	
				405					410					415		

Cys Cys Tyr Ser Gln Leu Ala Asn
420

<210> 89

<211> 1176

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1176)

<223> DORLU 24.1

<400> 89

atg tca aag cta atc gag gtg ttt ctg ggt aat ctg tgg acg cag cgt	48
Met Ser Lys Leu Ile Glu Val Phe Leu Gly Asn Leu Trp Thr Gln Arg	
1 5 10 15	
ttt acc ttc gcc cga atg ggt ttg gat ttg cag ccc gat aaa aag ggc	96
Phe Thr Phe Ala Arg Met Gly Leu Asp Leu Gln Pro Asp Lys Lys Gly	
20 25 30	
aat gtt ttg cga tct ccg ctt ctt tat tgt att atg tgt ctg aca aca	144
Asn Val Leu Arg Ser Pro Leu Leu Tyr Cys Ile Met Cys Leu Thr Thr	
35 40 45	
agc ttt gag ctc tgc acc gtg tgc gcc ttt atg gtc caa aat cgc aac	192
Ser Phe Glu Leu Cys Thr Val Cys Ala Phe Met Val Gln Asn Arg Asn	
50 55 60	
caa atc gtg ctt tgt tcc gag gcc ctg atg cac gga cta cag atg gtc	240
Gln Ile Val Leu Cys Ser Glu Ala Leu Met His Gly Leu Gln Met Val	
65 70 75 80	
tcc tcg cta ctg aag atg gct ata ttc ttg gcc aaa tct cac gac ctg	288
Ser Ser Leu Leu Lys Met Ala Ile Phe Leu Ala Lys Ser His Asp Leu	
85 90 95	
gtg gac cta att caa cag att cag tcg cct ttt aca gag gag gat ctt	336
Val Asp Leu Ile Gln Gln Ile Gln Ser Pro Phe Thr Glu Glu Asp Leu	
100 105 110	
gta ggt aca gag tgg aga tcc caa aat caa agg gga caa cta atg gct	384
Val Gly Thr Glu Trp Arg Ser Gln Asn Gln Arg Gly Gln Leu Met Ala	
115 120 125	

gcc att tac ttt atg atg tgt gcc ggt acg agt gtg tca ttt ctg ttg	432
Ala Ile Tyr Phe Met Met Cys Ala Gly Thr Ser Val Ser Phe Leu Leu	
130 135 140	
atg cca gtg gct ttg acc atg ctt aag tac cat tcc act ggg gaa ttc	480
Met Pro Val Ala Leu Thr Met Leu Lys Tyr His Ser Thr Gly Glu Phe	
145 150 155 160	
gcg cct gtc agc tcg ttc cgg gtt ctg ctt cca tac gat gtg aca caa	528
Ala Pro Val Ser Ser Phe Arg Val Leu Leu Pro Tyr Asp Val Thr Gln	
165 170 175	
ccg cat gtt tat gcc atg gac tgc tgc ttg atg gta ttt gtg tta agt	576
Pro His Val Tyr Ala Met Asp Cys Cys Leu Met Val Phe Val Leu Ser	
180 185 190	
ttt ttt tgc tgc tcc acc acc gga gtg gat acc tta tat gga tgg tgt	624
Phe Phe Cys Cys Ser Thr Thr Gly Val Asp Thr Leu Tyr Gly Trp Cys	
195 200 205	
gct tta ggc gtg agt tta caa tac cgt cgc ctc ggt caa caa ctt aaa	672
Ala Leu Gly Val Ser Leu Gln Tyr Arg Arg Leu Gly Gln Gln Leu Lys	
210 215 220	
agg ata ccc tcc tgt ttc aat cca tct cgg tct gac ttt gga tta agt	720
Arg Ile Pro Ser Cys Phe Asn Pro Ser Arg Ser Asp Phe Gly Leu Ser	
225 230 235 240	
ggg att ttt gtg gag cat gct cgt ctg ctt aaa ata gtc caa cat ttt	768
Gly Ile Phe Val Glu His Ala Arg Leu Leu Lys Ile Val Gln His Phe	
245 250 255	
aat tat agt ttt atg gag atc gca ttt gtg gag gtt gtt ata atc tgt	816
Asn Tyr Ser Phe Met Glu Ile Ala Phe Val Glu Val Val Ile Ile Cys	
260 265 270	
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Gly Leu Tyr Cys Ser Val Ile Cys Gln Tyr Ile Met Pro His Thr Asn	
275 280 285	
caa aac ttc gcc ttt ctg ggt ttc ttt tca ttg gta gtt acc aca cag	912
Gln Asn Phe Ala Phe Leu Gly Phe Phe Ser Leu Val Val Thr Thr Gln	
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Leu Cys Ile Tyr Leu Phe Gly Ala Glu Gln Val Arg Leu Glu Ala Glu	
305 310 315 320	

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 Pro Lys His Arg Lys Leu Phe Leu Phe Pro Ile Glu Arg Ala Gln Arg
 340 345 350

gaa act gtt ctc ggt gct tat ttc ttc gaa cta ggc aga cct ctt ctt 1104
 Glu Thr Val Leu Gly Ala Tyr Phe Phe Glu Leu Gly Arg Pro Leu Leu
 355 360 365

gtt tgg ata ttt cgc aca gca ggc tct ttt aca act ttg atg aac gct 1152
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 370 375 380

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 385 390

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 Asn Val Leu Arg Ser Pro Leu Leu Tyr Cys Ile Met Cys Leu Thr Thr
 35 40 45
 Ser Phe Glu Leu Cys Thr Val Cys Ala Phe Met Val Gln Asn Arg Asn
 50 55 60
 Gln Ile Val Leu Cys Ser Glu Ala Leu Met His Gly Leu Gln Met Val
 65 70 75 80
 Ser Ser Leu Leu Lys Met Ala Ile Phe Leu Ala Lys Ser His Asp Leu
 85 90 95
 Val Asp Leu Ile Gln Gln Ile Gln Ser Pro Phe Thr Glu Glu Asp Leu
 100 105 110

Val	Gly	Thr	Glu	Trp	Arg	Ser	Gln	Asn	Gln	Arg	Gly	Gln	Leu	Met	Ala	115	120	125	
Ala	Ile	Tyr	Phe	Met	Met	Cys	Ala	Gly	Thr	Ser	Val	Ser	Phe	Leu	Leu	130	135	140	
Met	Pro	Val	Ala	Leu	Thr	Met	Leu	Lys	Tyr	His	Ser	Thr	Gly	Glu	Phe	145	150	155	160
Ala	Pro	Val	Ser	Ser	Phe	Arg	Val	Leu	Leu	Pro	Tyr	Asp	Val	Thr	Gln	165	170	175	
Pro	His	Val	Tyr	Ala	Met	Asp	Cys	Cys	Leu	Met	Val	Phe	Val	Leu	Ser	180	185	190	
Phe	Phe	Cys	Cys	Ser	Thr	Thr	Gly	Val	Asp	Thr	Leu	Tyr	Gly	Trp	Cys	195	200	205	
Ala	Leu	Gly	Val	Ser	Leu	Gln	Tyr	Arg	Arg	Leu	Gly	Gln	Gln	Leu	Lys	210	215	220	
Arg	Ile	Pro	Ser	Cys	Phe	Asn	Pro	Ser	Arg	Ser	Asp	Phe	Gly	Leu	Ser	225	230	235	240
Gly	Ile	Phe	Val	Glu	His	Ala	Arg	Leu	Leu	Lys	Ile	Val	Gln	His	Phe	245	250	255	
Asn	Tyr	Ser	Phe	Met	Glu	Ile	Ala	Phe	Val	Glu	Val	Val	Ile	Ile	Cys	260	265	270	
Gly	Leu	Tyr	Cys	Ser	Val	Ile	Cys	Gln	Tyr	Ile	Met	Pro	His	Thr	Asn	275	280	285	
Gln	Asn	Phe	Ala	Phe	Leu	Gly	Phe	Phe	Ser	Leu	Val	Val	Thr	Thr	Gln	290	295	300	
Leu	Cys	Ile	Tyr	Leu	Phe	Gly	Ala	Glu	Gln	Val	Arg	Leu	Glu	Ala	Glu	305	310	315	320
Arg	Phe	Ser	Arg	Leu	Leu	Tyr	Glu	Val	Ile	Pro	Trp	Gln	Asn	Leu	Pro	325	330	335	
Pro	Lys	His	Arg	Lys	Leu	Phe	Leu	Phe	Pro	Ile	Glu	Arg	Ala	Gln	Arg	340	345	350	
Glu	Thr	Val	Leu	Gly	Ala	Tyr	Phe	Phe	Glu	Leu	Gly	Arg	Pro	Leu	Leu	355	360	365	

Val Trp Ile Phe Arg Thr Ala Gly Ser Phe Thr Thr Leu Met Asn Ala
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Leu Tyr Ala Lys Tyr Glu Thr His
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 Arg Asp Leu Phe Val Phe Val Arg Gln Thr Met Cys Ile Ala Ala Met
 20 25 30
 tat ccc ttc ggt tac tac gtg aat gga tct gga gtc ctg gcc gtt ctg 144
 Tyr Pro Phe Gly Tyr Tyr Val Asn Gly Ser Gly Val Leu Ala Val Leu
 35 40 45
 gtg cga ttc tgt gac ttg acc tac gag ctc ttt aac tac ttc gtt tcg 192
 Val Arg Phe Cys Asp Leu Thr Tyr Glu Leu Phe Asn Tyr Phe Val Ser
 50 55 60
 gta cac ata gct ggc ctg tac atc tgc acc atc tac atc aac tat ggg 240
 Val His Ile Ala Gly Leu Tyr Ile Cys Thr Ile Tyr Ile Asn Tyr Gly
 65 70 75 80
 caa ggc gat ttg gac ttc ttc gtg aac tgt ttg ata caa acc att att 288
 Gln Gly Asp Leu Asp Phe Phe Val Asn Cys Leu Ile Gln Thr Ile Ile
 85 90 95
 tat ctg tgg aca ata gcg atg aaa ctc tac ttt cgg agg ttc aga cct 336
 Tyr Leu Trp Thr Ile Ala Met Lys Leu Tyr Phe Arg Arg Phe Arg Pro
 100 105 110

ggt ttg ttg aat acc att ctg tcc aac atc aat gat gag tac gag aca	384
Gly Leu Leu Asn Thr Ile Leu Ser Asn Ile Asn Asp Glu Tyr Glu Thr	
115 120 125	
cggt tgc gct gtg gga ttc agt ttc gtc aca atg gcg gga tcc tat cgg	432
Arg Ser Ala Val Gly Phe Ser Phe Val Thr Met Ala Gly Ser Tyr Arg	
130 135 140	
atg tcc aag cta tgg atc aaa acc tat gtg tat tgc tgc tac ata ggc	480
Met Ser Lys Leu Trp Ile Lys Thr Tyr Val Tyr Cys Cys Tyr Ile Gly	
145 150 155 160	
acc att ttc tgg ctg gct ctt ccc att gcc tac cgg gat agg agt ctt	528
Thr Ile Phe Trp Leu Ala Leu Pro Ile Ala Tyr Arg Asp Arg Ser Leu	
165 170 175	
cct ctt gcc tgc tgg tat ccc ttt gac tat aca caa ccc ggt gtc tat	576
Pro Leu Ala Cys Trp Tyr Pro Phe Asp Tyr Thr Gln Pro Gly Val Tyr	
180 185 190	
gag gta gtg ttc ctt ctc cag gcg atg gga cag atc caa gtg gcc gca	624
Glu Val Val Phe Leu Leu Gln Ala Met Gly Gln Ile Gln Val Ala Ala	
195 200 205	
tcc ttt gcc tcc tcc agt ggc ctg cat atg gtg ctt tgt gtg ctg ata	672
Ser Phe Ala Ser Ser Ser Gly Leu His Met Val Leu Cys Val Leu Ile	
210 215 220	
tca ggg cag tac gat gtc ctc ttt tgc agt ctc aag aat gta tta gcc	720
Ser Gly Gln Tyr Asp Val Leu Phe Cys Ser Leu Lys Asn Val Leu Ala	
225 230 235 240	
agc agc tat gtc ctt atg gga gcc aat atg acg gaa ctg aat caa ttg	768
Ser Ser Tyr Val Leu Met Gly Ala Asn Met Thr Glu Leu Asn Gln Leu	
245 250 255	
cag gct gag caa tct gcg gcc gat gtc gag cca ggt cag tat gct tac	816
Gln Ala Glu Gln Ser Ala Ala Asp Val Glu Pro Gly Gln Tyr Ala Tyr	
260 265 270	
tcc gtg gag gag gag aca cct ttg caa gaa ctt cta aaa gtt ggg agc	864
Ser Val Glu Glu Glu Thr Pro Leu Gln Glu Leu Leu Lys Val Gly Ser	
275 280 285	
tca atg gac ttc tcc tcc gca ttc agg ctg tct ttt gtg cgg tgc att	912
Ser Met Asp Phe Ser Ser Ala Phe Arg Leu Ser Phe Val Arg Cys Ile	
290 295 300	

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Gln His His Arg Tyr	Ile Val Ala Ala Leu Lys Lys Ile Glu Ser Phe	
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Tyr Ser Pro Ile Trp Phe Val Lys Ile	Gly Glu Val Thr Phe Leu Met	
325	330 335	
tgc ctg gta gcc ttc gtc tcc acg aag agc acc gcg gcc aac tca ttc	1056	
Cys Leu Val Ala Phe Val Ser Thr Lys Ser Thr Ala Ala Asn Ser Phe		
340	345 350	
atg cga atg gtc tcc ttg ggc cag tac ctg ctc tta gtt ctc tac gag	1104	
Met Arg Met Val Ser Leu Gly Gln Tyr Leu Leu Leu Val Leu Tyr Glu		
355	360 365	
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Leu Phe Ile Ile Cys Tyr Phe Ala Asp Ile Val Phe Gln Asn Ser Gln		
370	375 380	
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Arg Cys Gly Glu Ala Leu Trp Arg Ser Pro Trp Gln Arg His Leu Lys		
385	390 395 400	
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Asp Val Arg Ser Asp Tyr Met Phe Phe Met Leu Asn Ser Arg Arg Gln		
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Phe Gln Leu Thr Ala Gly Lys Ile Ser Asn Leu Asn Val Asp Arg Phe		
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Met Asp Ala Arg Glu		
450		

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Arg Asp Leu Phe Val Phe Val Arg Gln Thr Met Cys Ile Ala Ala Met	20	25	30
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Val Arg Phe Cys Asp Leu Thr Tyr Glu Leu Phe Asn Tyr Phe Val Ser	50	55	60
Val His Ile Ala Gly Leu Tyr Ile Cys Thr Ile Tyr Ile Asn Tyr Gly	65	70	75
Gln Gly Asp Leu Asp Phe Phe Val Asn Cys Leu Ile Gln Thr Ile Ile	85	90	95
Tyr Leu Trp Thr Ile Ala Met Lys Leu Tyr Phe Arg Arg Phe Arg Pro	100	105	110
Gly Leu Leu Asn Thr Ile Leu Ser Asn Ile Asn Asp Glu Tyr Glu Thr	115	120	125
Arg Ser Ala Val Gly Phe Ser Phe Val Thr Met Ala Gly Ser Tyr Arg	130	135	140
Met Ser Lys Leu Trp Ile Lys Thr Tyr Val Tyr Cys Cys Tyr Ile Gly	145	150	155
Thr Ile Phe Trp Leu Ala Leu Pro Ile Ala Tyr Arg Asp Arg Ser Leu	165	170	175
Pro Leu Ala Cys Trp Tyr Pro Phe Asp Tyr Thr Gln Pro Gly Val Tyr	180	185	190
Glu Val Val Phe Leu Leu Gln Ala Met Gly Gln Ile Gln Val Ala Ala	195	200	205
Ser Phe Ala Ser Ser Ser Gly Leu His Met Val Leu Cys Val Leu Ile	210	215	220
Ser Gly Gln Tyr Asp Val Leu Phe Cys Ser Leu Lys Asn Val Leu Ala	225	230	235
Ser Ser Tyr Val Leu Met Gly Ala Asn Met Thr Glu Leu Asn Gln Leu	245	250	255
Gln Ala Glu Gln Ser Ala Ala Asp Val Glu Pro Gly Gln Tyr Ala Tyr			

260	265	270
Ser Val Glu Glu Glu Thr Pro Leu Gln Glu Leu Leu Lys Val Gly Ser		
275	280	285
Ser Met Asp Phe Ser Ser Ala Phe Arg Leu Ser Phe Val Arg Cys Ile		
290	295	300
Gln His His Arg Tyr Ile Val Ala Ala Leu Lys Lys Ile Glu Ser Phe		
305	310	315 320
Tyr Ser Pro Ile Trp Phe Val Lys Ile Gly Glu Val Thr Phe Leu Met		
	325	330 335
Cys Leu Val Ala Phe Val Ser Thr Lys Ser Thr Ala Ala Asn Ser Phe		
	340	345 350
Met Arg Met Val Ser Leu Gly Gln Tyr Leu Leu Leu Val Leu Tyr Glu		
	355	360 365
Leu Phe Ile Ile Cys Tyr Phe Ala Asp Ile Val Phe Gln Asn Ser Gln		
	370	375 380
Arg Cys Gly Glu Ala Leu Trp Arg Ser Pro Trp Gln Arg His Leu Lys		
385	390	395 400
Asp Val Arg Ser Asp Tyr Met Phe Phe Met Leu Asn Ser Arg Arg Gln		
	405	410 415
Phe Gln Leu Thr Ala Gly Lys Ile Ser Asn Leu Asn Val Asp Arg Phe		
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Gln Asp Val Val His Ile Val Ile Ser Ile Met Ser Glu Trp Leu Arg	
20 25 30	
ttt ctg aaa cgc gat caa cag ctg gat gtg tac ttt ttt gca gtg ccc	144
Phe Leu Lys Arg Asp Gln Gln Leu Asp Val Tyr Phe Phe Ala Val Pro	
35 40 45	
cgc ttg agt tta gac ata atg ggc tat tgg ccg ggc aaa act ggt gat	192
Arg Leu Ser Leu Asp Ile Met Gly Tyr Trp Pro Gly Lys Thr Gly Asp	
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aca tgg ccc tgg aga tcc ctg att cac ttc gca atc ctg gcc att ggc	240
Thr Trp Pro Trp Arg Ser Leu Ile His Phe Ala Ile Leu Ala Ile Gly	
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gtg gcc acc gaa ctg cat gct ggc atg tgt ttt cta gac cga cag cag	288
Val Ala Thr Glu Leu His Ala Gly Met Cys Phe Leu Asp Arg Gln Gln	
85 90 95	
att acc ttg gca ctg gag acc ctc tgt cca gct ggc aca tcg gcg gtc	336
Ile Thr Leu Ala Leu Glu Thr Leu Cys Pro Ala Gly Thr Ser Ala Val	
100 105 110	
acg ctg ctc aag atg ttc cta atg ctg cgc ttt cgt cag gat ctc tcc	384
Thr Leu Leu Lys Met Phe Leu Met Leu Arg Phe Arg Gln Asp Leu Ser	
115 120 125	
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Ile Met Trp Asn Arg Leu Arg Gly Leu Leu Phe Asp Pro Asn Trp Glu	
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cga ccc gag cag cgg gac atc cgg cta aag cac tcg gcc atg gcg gct	480
Arg Pro Glu Gln Arg Asp Ile Arg Leu Lys His Ser Ala Met Ala Ala	
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Arg Ile Asn Phe Trp Pro Leu Ser Ala Gly Phe Phe Thr Cys Thr Thr	
165 170 175	
tac aac cta aag ccg ata ctg atc gca atg ata ttg tat ctc cag aat	576

Tyr Asn Leu Lys Pro Ile Leu Ile Ala Met Ile Leu Tyr Leu Gln Asn	
180	185 190
cgt tac gag gac ttc gtt tgg ttt aca ccc ttc aat atg act atg ccc	624
Arg Tyr Glu Asp Phe Val Trp Phe Thr Pro Phe Asn Met Thr Met Pro	
195 200 205	
aaa gtt ctg cta aac tat cca ttt ttt ccc ctg acc tac ata ttt att	672
Lys Val Leu Leu Asn Tyr Pro Phe Phe Pro Leu Thr Tyr Ile Phe Ile	
210 215 220	
gcc tat acg ggc tat gtg acc atc ttt atg ttc ggc ggc tgt gat ggt	720
Ala Tyr Thr Gly Tyr Val Thr Ile Phe Met Phe Gly Gly Cys Asp Gly	
225 230 235 240	
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Phe Tyr Phe Glu Phe Cys Ala His Leu Ser Ala Leu Phe Glu Val Leu	
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Gln Ala Glu Ile Glu Ser Met Phe Arg Pro Tyr Thr Asp His Leu Glu	
260 265 270	
ctg tcg cca gtg cag ctt tac att tta gag caa aag atg cga tca gta	864
Leu Ser Pro Val Gln Leu Tyr Ile Leu Glu Gln Lys Met Arg Ser Val	
275 280 285	
atc att agg cac aat gcc atc atc gat ttg acc aga ttt ttt cgt gat	912
Ile Ile Arg His Asn Ala Ile Ile Asp Leu Thr Arg Phe Phe Arg Asp	
290 295 300	
cgc tat acc att att acc ctg gcc cat ttt gtg tcc gcc gcc atg gtg	960
Arg Tyr Thr Ile Ile Thr Leu Ala His Phe Val Ser Ala Ala Met Val	
305 310 315 320	
att gga ttc agc atg gtt aat ctc ctg aca ttg ggc aat aat ggt ctg	1008
Ile Gly Phe Ser Met Val Asn Leu Leu Thr Leu Gly Asn Asn Gly Leu	
325 330 335	
ggc gca atg ctc tat gtg gcc tac acg gtt gcc gct ttg agc caa ctg	1056
Gly Ala Met Leu Tyr Val Ala Tyr Thr Val Ala Ala Leu Ser Gln Leu	
340 345 350	
ctg gtt tat tgc tat ggc gga act ctg gtg gcc gaa agt agc act ggt	1104
Leu Val Tyr Cys Tyr Gly Gly Thr Leu Val Ala Glu Ser Ser Thr Gly	
355 360 365	
ctg tgc cga gcc atg ttc tcc tgt ccg tgg cag ctt ttt aag cct aaa	1152

Leu Cys Arg Ala Met Phe Ser Cys Pro Trp Gln Leu Phe Lys Pro Lys
 370 375 380

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 Gln Arg Arg Leu Val Gln Leu Leu Ile Leu Arg Ser Gln Arg Pro Val
 385 390 395 400

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 Ser Met Ala Val Pro Phe Phe Ser Pro Ser Leu Ala Thr Phe Ala Ala
 405 410 415

 att ctt caa act tcg ggt tcc ata att gcg ctg gtt aag tcc ttt cag 1296
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 <213> *Drosophila melanogaster*

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 35 40 45

 Arg Leu Ser Leu Asp Ile Met Gly Tyr Trp Pro Gly Lys Thr Gly Asp
 50 55 60

 Thr Trp Pro Trp Arg Ser Leu Ile His Phe Ala Ile Leu Ala Ile Gly
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 Val Ala Thr Glu Leu His Ala Gly Met Cys Phe Leu Asp Arg Gln Gln
 85 90 95

 Ile Thr Leu Ala Leu Glu Thr Leu Cys Pro Ala Gly Thr Ser Ala Val
 100 105 110

 Thr Leu Leu Lys Met Phe Leu Met Leu Arg Phe Arg Gln Asp Leu Ser
 115 120 125

 Ile Met Trp Asn Arg Leu Arg Gly Leu Leu Phe Asp Pro Asn Trp Glu
 130 135 140

Arg	Pro	Glu	Gln	Arg	Asp	Ile	Arg	Leu	Lys	His	Ser	Ala	Met	Ala	Ala	145	150	155	160
Arg	Ile	Asn	Phe	Trp	Pro	Leu	Ser	Ala	Gly	Phe	Phe	Thr	Cys	Thr	Thr	165	170	175	
Tyr	Asn	Leu	Lys	Pro	Ile	Leu	Ile	Ala	Met	Ile	Leu	Tyr	Leu	Gln	Asn	180	185	190	
Arg	Tyr	Glu	Asp	Phe	Val	Trp	Phe	Thr	Pro	Phe	Asn	Met	Thr	Met	Pro	195	200	205	
Lys	Val	Leu	Leu	Asn	Tyr	Pro	Phe	Phe	Pro	Leu	Thr	Tyr	Ile	Phe	Ile	210	215	220	
Ala	Tyr	Thr	Gly	Tyr	Val	Thr	Ile	Phe	Met	Phe	Gly	Gly	Cys	Asp	Gly	225	230	235	240
Phe	Tyr	Phe	Glu	Phe	Cys	Ala	His	Leu	Ser	Ala	Leu	Phe	Glu	Val	Leu	245	250	255	
Gln	Ala	Glu	Ile	Glu	Ser	Met	Phe	Arg	Pro	Tyr	Thr	Asp	His	Leu	Glu	260	265	270	
Leu	Ser	Pro	Val	Gln	Leu	Tyr	Ile	Leu	Glu	Gln	Lys	Met	Arg	Ser	Val	275	280	285	
Ile	Ile	Arg	His	Asn	Ala	Ile	Ile	Asp	Leu	Thr	Arg	Phe	Phe	Arg	Asp	290	295	300	
Arg	Tyr	Thr	Ile	Ile	Thr	Leu	Ala	His	Phe	Val	Ser	Ala	Ala	Met	Val	305	310	315	320
Ile	Gly	Phe	Ser	Met	Val	Asn	Leu	Leu	Thr	Leu	Gly	Asn	Asn	Gly	Leu	325	330	335	
Gly	Ala	Met	Leu	Tyr	Val	Ala	Tyr	Thr	Val	Ala	Ala	Leu	Ser	Gln	Leu	340	345	350	
Leu	Val	Tyr	Cys	Tyr	Gly	Gly	Thr	Leu	Val	Ala	Glu	Ser	Ser	Thr	Gly	355	360	365	
Leu	Cys	Arg	Ala	Met	Phe	Ser	Cys	Pro	Trp	Gln	Leu	Phe	Lys	Pro	Lys	370	375	380	
Gln	Arg	Arg	Leu	Val	Gln	Leu	Leu	Ile	Leu	Arg	Ser	Gln	Arg	Pro	Val	385	390	395	400

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Leu Leu Pro Tyr Arg Ser Lys Trp His Thr Leu Val Tyr Ile Gln Met
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gtt ata ttt ttt gct tca atg agc ttt ggc tta acg gaa tcg atg gga 144
Val Ile Phe Phe Ala Ser Met Ser Phe Gly Leu Thr Glu Ser Met Gly
35 40 45

gac cat gtt caa atg gga cgg gac tta gcc ttc atc ctt ggg aca tat 192
Asp His Val Gln Met Gly Arg Asp Leu Ala Phe Ile Leu Gly Thr Tyr
50 55 60

tat ttc tgc tgg tat ggc gat gaa ctt gac caa gtg atc agc gat ctg 240
Tyr Phe Cys Trp Tyr Gly Asp Glu Leu Asp Gln Val Ile Ser Asp Leu
65 70 75 80

gac gct cta cat cct tgg gca cag aaa ggt cct aat cca gtt gaa tat 288
Asp Ala Leu His Pro Trp Ala Gln Lys Gly Pro Asn Pro Val Glu Tyr
85 90 95

cag act ggt aaa cgt tgg tac ttc gta atg gct ttt ttc ttg gca acg 336
Gln Thr Gly Lys Arg Trp Tyr Phe Val Met Ala Phe Phe Leu Ala Thr
100 105 110

tca tgg tcg ttc ttc ttg tgc att ttg cta ttg tta ctt ata acc tca	384
Ser Trp Ser Phe Phe Leu Cys Ile Leu Leu Leu Leu Leu Ile Thr Ser	
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ccc atg tgg gtc cat cag caa aac ctt ccc ttt cat gcg gcg ttt cct	432
Pro Met Trp Val His Gln Gln Asn Leu Pro Phe His Ala Ala Phe Pro	
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ttt caa tgg cac gaa aaa tcg ctt cat ccc atc agc cac gct ata atc	480
Phe Gln Trp His Glu Lys Ser Leu His Pro Ile Ser His Ala Ile Ile	
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tgc ata gag gga cta tca att tgt att tat gcg gaa att act ttc ggc	576
Cys Ile Glu Gly Leu Ser Ile Cys Ile Tyr Ala Glu Ile Thr Phe Gly	
180 185 190	
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Ile Glu Val Leu Cys Leu Glu Leu Arg Gln Ile His Arg His Asn Tyr	
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Gly Leu Gln Glu Leu Arg Met Glu Thr Asn Arg Leu Val Lys Leu His	
210 215 220	
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Gln Lys Ile Met Gly Val Asn Phe Ser Leu Val Ser Leu Ser Val Leu	
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Glu Ala Val Glu Ala Arg Lys Asp Pro Lys Val Val Ala Gln Phe Ala	
245 250 255	
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Val Leu Met Leu Leu Ala Leu Gly His Leu Ser Met Trp Ser Tyr Cys	
260 265 270	
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Gly Asp Gln Leu Ser Gln Lys Ser Leu Gln Ile Ser Glu Ala Ala Tyr	
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Glu Ala Tyr Asp Pro Thr Lys Gly Ser Lys Asp Val Tyr Arg Asp Leu	
290 295 300	

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 Cys Val Ile Ile Arg Arg Gly Gln Asp Pro Leu Ile Met Arg Ala Ser
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Tyr Phe Cys Trp Tyr Gly Asp Glu Leu Asp Gln Val Ile Ser Asp Leu
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Asp Ala Leu His Pro Trp Ala Gln Lys Gly Pro Asn Pro Val Glu Tyr
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Gln Thr Gly Lys Arg Trp Tyr Phe Val Met Ala Phe Phe Leu Ala Thr
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Ser Trp Ser Phe Phe Leu Cys Ile Leu Leu Leu Leu Ile Thr Ser
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Phe Gln Trp His Glu Lys Ser Leu His Pro Ile Ser His Ala Ile Ile
 145 150 155 160

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Cys	Ile	Glu	Gly	Leu	Ser	Ile	Cys	Ile	Tyr	Ala	Glu	Ile	Thr	Phe	Gly	180	185	190	
Ile	Glu	Val	Leu	Cys	Leu	Glu	Leu	Arg	Gln	Ile	His	Arg	His	Asn	Tyr	195	200	205	
Gly	Leu	Gln	Glu	Leu	Arg	Met	Glu	Thr	Asn	Arg	Leu	Val	Lys	Leu	His	210	215	220	
Gln	Lys	Ile	Met	Gly	Val	Asn	Phe	Ser	Leu	Val	Ser	Leu	Ser	Val	Leu	225	230	235	240
Glu	Ala	Val	Glu	Ala	Arg	Lys	Asp	Pro	Lys	Val	Val	Ala	Gln	Phe	Ala	245	250	255	
Val	Leu	Met	Leu	Leu	Ala	Leu	Gly	His	Leu	Ser	Met	Trp	Ser	Tyr	Cys	260	265	270	
Gly	Asp	Gln	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Ile	Ser	Glu	Ala	Ala	Tyr	275	280	285	
Glu	Ala	Tyr	Asp	Pro	Thr	Lys	Gly	Ser	Lys	Asp	Val	Tyr	Arg	Asp	Leu	290	295	300	
Cys	Val	Ile	Ile	Arg	Arg	Gly	Gln	Asp	Pro	Leu	Ile	Met	Arg	Ala	Ser	305	310	315	320
Pro	Phe	Pro	Ser	Phe	Asn	Leu	Ile	Asn	Tyr	Ser	Ala	Ile	Leu	Asn	Gln	325	330	335	
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Thr Leu Lys Leu Met Lys Phe Trp Ser Tyr Leu Phe Val His Asn Trp	
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cgc cgc tat gtc gca atg act ccg tac atc att atc aac tgt act cag	144
Arg Arg Tyr Val Ala Met Thr Pro Tyr Ile Ile Ile Asn Cys Thr Gln	
35 40 45	
tat gtg gat ata tat ctg agc acc gaa tcc ttg gac ttt atc atc aga	192
Tyr Val Asp Ile Tyr Leu Ser Thr Glu Ser Leu Asp Phe Ile Ile Arg	
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Leu Leu Cys Val Gln Arg Phe Ser Tyr Glu Arg Phe Ile Asn Ile Leu	
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Lys Ser Phe Tyr Ile Glu Leu Leu Gln Ser Asp Asp Pro Ile Ile Asn	
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Ile Leu Val Lys Glu Thr Thr Arg Leu Ser Val Leu Ile Ser Arg Ile	
115 120 125	
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Asn Leu Leu Met Gly Cys Cys Thr Cys Ile Gly Phe Val Thr Tyr Pro	
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Ile Phe Gly Ser Glu Arg Val Leu Pro Tyr Gly Met Tyr Leu Pro Thr	
145 150 155 160	
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Ile Asp Glu Tyr Lys Tyr Ala Ser Pro Tyr Tyr Glu Ile Phe Phe Val	
165 170 175	
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Ile Gln Ala Ile Met Ala Pro Met Gly Cys Cys Met Tyr Ile Pro Tyr	

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Thr Asn Met Val Val Thr Phe Thr Leu Phe Ala Ile Leu Met Cys Arg			
195	200	205	
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Val Leu Gln His Lys Leu Arg Ser Leu Glu Lys Leu Lys Asn Glu Gln			
210	215	220	
gta cgt ggt gaa atc ata tgg tgc ata aaa tat caa tta aaa tta tca			720
Val Arg Gly Glu Ile Ile Trp Cys Ile Lys Tyr Gln Leu Lys Leu Ser			
225	230	235	240
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Gly Phe Val Asp Ser Met Asn Ala Leu Asn Thr His Leu His Leu Val			
245	250	255	
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Glu Phe Leu Cys Phe Gly Ala Met Leu Cys Val Leu Leu Phe Ser Leu			
260	265	270	
ata att gct caa aca att gct cag acc gtc ata gtc atc gca tac atg			864
Ile Ile Ala Gln Thr Ile Ala Gln Thr Val Ile Val Ile Ala Tyr Met			
275	280	285	
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Val Met Ile Phe Ala Asn Ser Val Val Leu Tyr Tyr Val Ala Asn Glu			
290	295	300	
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aag tat ggg att ttg cag agc ttt gat att gcc att gct gcc tat gag			1008
Lys Tyr Gly Ile Leu Gln Ser Phe Asp Ile Ala Ile Ala Ala Tyr Glu			
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Ser Asn Trp Met Asp Phe Asp Val Asp Thr Gln Lys Thr Leu Lys Phe			
340	345	350	
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Leu Ile Met Arg Ser Gln Lys Pro Leu Ala Thr Leu Val Gly Gly Thr			
355	360	365	
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Tyr Pro Met Asn Leu Lys Met Leu Gln Ser Leu Leu Asn Ala Ile Tyr			

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380

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30

Arg Arg Tyr Val Ala Met Thr Pro Tyr Ile Ile Ile Asn Cys Thr Gln

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Tyr Val Asp Ile Tyr Leu Ser Thr Glu Ser Leu Asp Phe Ile Ile Arg

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60

Asn Val Tyr Leu Ala Val Leu Phe Thr Asn Thr Val Val Arg Gly Val

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70

75

80

Leu Leu Cys Val Gln Arg Phe Ser Tyr Glu Arg Phe Ile Asn Ile Leu

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90

95

Lys Ser Phe Tyr Ile Glu Leu Leu Gln Ser Asp Asp Pro Ile Ile Asn

100

105

110

Ile Leu Val Lys Glu Thr Thr Arg Leu Ser Val Leu Ile Ser Arg Ile

115

120

125

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130

135

140

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145

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155

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165

170

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 210 215 220

Val Arg Gly Glu Ile Ile Trp Cys Ile Lys Tyr Gln Leu Lys Leu Ser
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Gly Phe Val Asp Ser Met Asn Ala Leu Asn Thr His Leu His Leu Val
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Glu Phe Leu Cys Phe Gly Ala Met Leu Cys Val Leu Leu Phe Ser Leu
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Leu Tyr Phe Gln Val Arg Val Val Gln Phe Ser Phe Lys Phe Leu Tyr
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Lys Tyr Gly Ile Leu Gln Ser Phe Asp Ile Ala Ile Ala Ala Tyr Glu
 325 330 335

Ser Asn Trp Met Asp Phe Asp Val Asp Thr Gln Lys Thr Leu Lys Phe
 340 345 350

Leu Ile Met Arg Ser Gln Lys Pro Leu Ala Thr Leu Val Gly Gly Thr
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<222> (844)..(918)

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<222> (852)..(930)

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